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Mutant alpha-amylase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for use in detergents, dishwashing agents and liquefaction agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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AAP81180
AAR07574
AAR65107
AAR66109
AAP17605
AAW17607
AAW17595
AAW17595
AAW17595
AAW17596
                                                                                      ADS44249
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92DK-00001503.
93DK-00000292.
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(first entry)
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   23-JUL-1992;
16-DEC-1992;
15-MAR-1993;
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18-JUL-1994
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Aau14500
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Searched:

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Oxidation stable alpha amylases can be used for the simultaneous desizing and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or Asp. The parent alpha amylase is pref. derived from a Bacillus species, although alpha amylases of fungal origin can also be used. This sequence is the wild type (unmodified) alpha amylase of Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of an oxidation stable alpha-amylase - for simultaneous desizing and bleaching or scouring of fabrics contg. starch or starch derivs.
                                                                                                                 Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch; thermostable; methionine; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl; Aspergillus oryzae; Bacillus amyloliquefaciens; altered property; calcium dependency; substrate binding; stability; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction; sweetener; ethanol production; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 78; DB 2; Length 478; 100.0%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus oryzae alpha-amylase (mature protein).
                                                                                    oryzae alpha amylase (mature protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nilsson TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 25-26; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pedersen HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW14500 standard; protein; 478 AA.
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                                                                                                                                                                                                                                                                                                                                                                        94DK-00000141
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                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 AYHGYWQQDIYSL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toft AH, Marcher D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-283767/37.
                                                                                                                                                                                  Aspergillus oryzae.
                                                                                                                                                                                                                   Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                   05-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                        02-FEB-1994;
                                                                                                                                                                                                                                                          W09521247-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUN-1997
                                                  17-JAN-1996
                                                                                    Aspergillus
                                                                                                                                                                                                                                                                                                10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW14500;
             AAR78270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, bleaching and dyeing. The variants have improved thermostability, acid/alkaline stability; low temperature optimum; pH optimum; higher hydrolysis velocity and improved colerance to obtain composition constituents, e.g. oxidation agents. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Bacillus derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 78; DB 2; Length 478; 100.0%; Pred. No. 0.0011;
                               Score 78; DB 2; Length 478; Pred. No. 0.0011; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                          Aspergillus oryzae alpha amylase (mature protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bisgard-Frantzen H, Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 75-76; 105pp; English.
                                                                                                                                                                                                                                             AAR72450 standard; protein; 478 AA.
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0
                                     100.0%;
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94DK-00000140.
                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
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                                                                                                           1 AYHGYWQQDIYSL 13
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                                   Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-161790/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus oryzae.
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les 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 478 AA;
Seguence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9510603-A1
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                                                                                                                                                                                                                                                                                                                   25-MAR-2003
01-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-1995
                                                                                                                                                                                                                                                                                AAR72450;
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Gaps

.. 0

AAR78270 standard; protein; 478 AA.

AAR78270 RESULT 3

Matches

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The control of the corresponding to this region is deleted from the parent sequence of a variant region is deleted from the parent sequence of a variant Fungamy; claim 43"

291. 313

/label= loop 8 modification region
/note= "at least one amino acid residue of a parent alpha amylase (used as a template for a variant) corresponding fragment corresponding to this fragment; claim 36"
                                                                                                                                                                                                                                                                                                                                                  /label=loop 8 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 305-345 of AAW14498 is
deleted or replaced with a fragment corresponding to this
         residue of a parent alpha-amylase (used as a template for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the mature Aspergillus oryzae alpha-amylase (A). Variants of parent termamyl- and fungamyl-like alpha-amylases (and methods of constructing them) are claimed. Examples of variants are featured above. The variants have altered properties such as calcium dependency, substrate binding and stability. Also one or more proline or cysteine residues in the variant is modified or replaced with a non-proline or non-cystein residue such as alanine. The variants can be used for (dish) washing, as detergent additives or for fabric desizing or starch liquefaction. They can also be used for the production of sweeteners and ethanol from starch. See also AAW14498-99

    have altered
binding and stability.

                          a variant) corresponding to 196-198 of AAW14499 is deleted or replaced with a fragment corresponding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-amylase variants and methods of production properties such as calcium dependency, substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borchert TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 87-88; 171pp; English
                                                                      ragment; claim 23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fragment; claim 38"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Svendsen A, Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95DK-00000128.
95DK-00001192.
95DK-00001256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-DK000057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYHGYWQQDIYSL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AYHGYWQQDIYSL
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Best Local Similarity
                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9623874-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
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                     13. .45
/label= loop 1 modification region
/label= loop 1 modification acid residue of a parent alpha
-lamylase (used as template for a variant) corresponding
to 7-23 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 33"
                                                                                                                                                                                /label= loop 1 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 8-18 of AAW14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                               /label= loop 1 modification region
hore= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 12-19 of AAW14499 is deleted or replaced with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66. .84
/label= loop 2 modification region
/label= loop 2 modification region
/label= at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 44-57 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "preferred region where at least one amino acid residue of a parent alpha amylase (used as a template for a variant) corresponding to 48-51 of AAM14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98. .210
/label= loop 3 modification region
/label= loop 3 modification acid residue of a parent alpha
-amylase (used as template for a variant) corresponding
to 117-185 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-199 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 121-181 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "at least one amino acid residue of a parent alpha -amylase (used as a template for a variant) corresponding to 195-202 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "at least one amino acid residue of a parent alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 14-15 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -amylase (used as a template for a variant) correspondir to this fragment is deleted or replaced with a fragment corresponding to 102-206 of AAW14499; claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= loop 3 modification region
/note= "preferred region where at least one amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment corresponding to this fragment; claim 30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32. 38
/label= loop 1 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70. .78
/label= loop 2 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102. .206
/label= loop 3 modification region
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  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ragment; claim 32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragment; claim 26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166. .173
/label= lo
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                                                                                                                                                               .40
Key
Misc-difference
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Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance of glucomylase (glaA) and recovering heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase A (amyA) protein.
                                                                                                                                                                                                                             Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 78; DB 8; Length 498; 100.0%; Pred. No. 0.0011; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus niger neutral alpha-amylase B (amyB) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
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                                                                                                                                                                                                                                                                                                                                          Example 11; SEQ ID NO 22; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADT89628 standard; protein; 499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVOZYMES BIOTECH INC.
                                                                                      (NOVO ) NOVOZYMES BIOTECH INC.
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31-MAR-2004; 2004US-00815495.
                                            31-MAR-2003; 2003US-0459902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYHGYWQQDIYSL 111
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Best Local 3; Conservative
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N-PSDB; ADT89627.
                                                                                                                                                                      WPI; 2004-708545/69.
N-PSDB; ADT89631.
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                                                                                                                                Connelly M, Brody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004191864-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-2004
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                                                                                                                                                                                                                                                                                                      substance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a fungamyl-like alpha-amylase. The specification describes variants of this fungamyl-like alpha-amylase, which have an alteration in one the amino acid regions 98-110, 150-160, 151-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or substitution of an amino acid or an insertion of an amino acid downstream of a particular position. The variants retain alpha-amylase activity, and have better heat stability and/or stability at acidic pH, relative to wild-type enzyme. The variants can therefore be used at higher comperatures (more efficient conversion or faster reaction, and have reduced need for cooling and reduced risk of contamination). The variants of glucoamylase during dextrinisation. The variants are used to produce syrups, particularly of high maltose content, or alcohol, from starch; as dough improver for baked goods; in brewing, to increase fermentability of the wort; and for liquefaction of starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variant of Fungamyl-like alpha-amylase, useful for production of maltose syrups, includes mutations that improve stability against heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                              Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose; alcohol; starch; dough improver; brewing; starch liquification.
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    Amino acid sequence of a fungamyl-like alpha-amylase.
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                                                                                                                                                                                                                                                                                                                                                                         Pedersen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 42-45; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Svendsen A,
                                                                                                                                                                                                                                             10-NOV-2000; 2000WO-DK000626
                                                                                                                                                                                                                                                                                       99DK-00001617
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                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-367478/38.
N-PSDB; AAF90208.
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Best Local Similarity
Matches 13; Conserv
                                                                                                            Aspergillus oryzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 498 AA;
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                                                                                                                                                           WO200134784-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and acidic pH
                                                                                                                                                                                                                                                                                       10-NOV-1999;
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RESULT 6 ADT89632

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Gaps

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The present invention relates to a method of producing heterologous halological substance. The method involves culturing mutant of wild-type happergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide sequences comprising medification of glucoamylase (glash) and recovering heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase B (amyB) protein.

Sequence 499 AA;

; 0 100.0%; Score 78; DB 8; Length 499; 100.0%; Pred. No. 0.0011; ive 0; Mismatches 0; Indels 1 AYHGYWQQDIYSL 13 13; Conservative Local Similarity Query Match Matches δ

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Gaps

AYHGYWQQDIYSL 111 66

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RESULT 8

ABP96630 standard; protein; 1095 AA. 02-JUN-2003 ABP96630; 

(first entry)

Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.

Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch; maltodextrin; ethanol; fermentation; beverage; enzyme.

Aspergillus shirousami

Synthetic.

WO2003018766-A2

06-MAR-2003

27-AUG-2002; 2002WO-US027129

27-AUG-2001; 2001US-0315281P.

(SYGN ) SYNGENTA PARTICIPATIONS

Batie CJ, Chen W, Craig J, Kinkema M; Lanahan MB, Basu SS,

WPI; 2003-268420/26.

N-PSDB; ACC44572.

Novel polynucleotide encoding hyperthermophilic processing enzymes e.g. alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.

Claim 1; Page 107; 158pp; English

The present invention describes polynucleotides which encode processing enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose enzymes (e.g. alpha-amylase) that are optimised for expression in plants. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic processing enzymes, which are activated under suitable conditions to act pubor the desired substrate. Also described are self-processing transgenic plants and plant parts, e.g. grain, which express one or more of these enzymes and have an altered composition that facilitates plant and grain processing. Also described is a method (M) for converting starch to atach-derived products in a transformed plant part (TPP), by activating the starch processing enzyme contained in it. Transgenic grain is useful for preparing maltodextrin. A transformed plant (TP) can be used to produce food products having improved taste and to produce fermentable

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 (M) eliminates the need
              to mill or physically disrupt the integrity of plant parts prior to recovery of starch-derived products. The present sequence represents alpha-amylase/glucoamylase fusion protein, which is given in the exemplification of the present invention
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                                                                                                                                        Length 1095;
                                                                                                                                                                       0; Indels
substrates for ethanol and fermented beverages.
                                                                                                                                     100.0%; Score 78; DB 6; 100.0%; Pred. No. 0.0025;
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Best Local Similarity
                                                                                                      Sequence 1095 AA;
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RESULT 9

ABB80177 standard; protein; 495 AA. ABB8017

ABB80177;

(first entry) 11-AUG-2003

A. fumigatus AfAAL1

beta-galactosidase; invertase; lipase; alpha-amylase; laccase; polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; maltodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability. Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;

Aspergillus fumigatus.

WO2003012071-A2.

13-FEB-2003.

05-AUG-2002; 2002WO-US024842.

03-AUG-2001; 2001US-0309870P.

(ELIT-) ELITRA PHARM INC

WPI; 2003-332729/31

Ξ Bussey

Roemer T,

Jiang B, Storms R,

N-PSDB; ABQ80345, ABQ80346.

Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents.

Claim 17; Page 134-35; 169pp; English.

The sequences given in ABBB0164-87 show enzymatic proteins derived from A. fumigatus. These proteins display the catalytic activity of an enzyme such as tannase, callulase, glucose oxidase, glucoamylase, phytase, betagalactosidases, invertase, lipase, alpha-amylase, laccase, polygalacturonase or xylanase. Compositions comprising the tannase are useful for modulating the amount of compounds that composition. Compositions comprising the amount of cellulose in a composition. Compositions comprising glucose oxidase are useful for modulating the amount of myo-inositol phosphates in a composition. Compositions comprising comprising the amount of macount of modulating the amount of composition. Compositions comprising comprising the amount of lactose in a composition. Compositions comprising comprising the amount of sucrose in a composition. Composition of comprising the amount of sucrose in a composition. Composition of sucrose in a composition. Composition of sucrose in a composition comprising the amount of sucrose in a composition of sucrose in a composition.

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modulating the amount of glyceride in a composition. Compositions comprising alpha-amylases are useful for modulating the amount of starches or maltodextrins in a composition. Compositions comprising laccase are useful for modulating the amount of oxidated phenolic compounds in a composition. Compositions comprising polygalacturonases are useful for modulating the amount of high or low molecular weight polygalacturonic acid chains in a composition. Compositions comprising polygalacturonases are useful for modulating the amount of xylan or xylo-oligomers in a composition. The A. fundiating the amount of xylan or xylo-oligomers in a composition. The A. fundiating proteins and corresponding DNA's are useful in various industries such as those involved in the making of food and feed, beverages, textiles such as those involved in the making of food and feed, beverages, textiles and detergents. The DNA's are useful to express recombinant enzymes for characterization, modification or industrial uses, to compare with the nucleotide sequence of A.funigatus to identify duplicated genes of paralogs having the same or similar blochemical activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify contained or distant fungal organisms to identify patterns, and to raise anti-protein antibodies. The polypeptide having cannase activity increases the yield of tea liquor from tea leaves, improves the colour, flavour and health benefite of tea products, particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes manufacturing maltogenic amylase (EC 3.2.1.133) having improved transglycosylation activity, comprising using crystallisation and the three dimensional structure of maltogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus sp. IM6501, maltogenic amylase; EC 3.2.1.133; crystallisation; protein co-ordinate data; 3 dimensional structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75; DB 6; Length 495;
Pred. No. 0.0032;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus oryzae TAKA protein (TAA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB09072 standard; protein; 423 AA.
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(SAMY-) SAMYANG GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 AYHGYWQQDIYSV 109
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hes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 495 AA;
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Matches
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cc amylase. Manufacturing maltogenic amylase comprises the following steps:

(i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC 5027BP) and inserting the gene into plasmid put119 to construct crecombinant DNA (pThMA119); (ii) inserting the recombinant DNA to Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius of Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius con Dotain a microbial cell; (iii) suspending the microbial cell with buffer colution at pH 7.5 and obtaining supernatant; and (iv) passing the colution at pH 7.5 and obtaining supernatant; and (iv) passing the contionant through column chromatography and obtaining purified complexed. The maltogenic amylase is a dimer comprised of two maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase (ThMA) crystal. The amylase has a structure containing an activated cregion that consists of amino acid residues of Asp. 228, Glu-357, Asp-424, CC region that consists of amino acid residues of amino acid residues of millo and Hisliso. The present sequence represents Aspergillus oryzae TAKA containing in comparison with ThMA in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide from a filamentous fungus, preferably Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Folkers U, Albermann K, Hopper
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of an alpha-amylase of Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                   89.7%; Score 70; DB 4; Length 423; 92.3%; Pred. No. 0.016; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 61-63; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP97894 standard; protein; 494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          niger, useful in a baking process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-2001; 2001EP-00000379.
16-AUG-2001; 2001EP-0000380.
16-AUG-2001; 2001EP-00000381.
16-AUG-2001; 2001EP-00000382.
16-AUG-2001; 2001EP-00000383.
16-AUG-2001; 2001EP-00000384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maier D, Stock A, Wagner C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2002; 2002WO-NL000522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 AMHGYWOODIYSL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-312758/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                 Sequence 423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003016535-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP97894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP97894
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            8
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Matches

δ g AAR8821

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A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS 224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562) isolated from a T. lanuginosus gene library. The recombinant enzyme (54-60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7 and is active at 60-80 deg. (Updated on 16-0CT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermophilic alpha-amylase with activity range of 60-80 degrees C -derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs and bakery prods. esp. bread.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                             Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.5%; Score 69; DB 2; Length 493; 76.9%; Pred. No. 0.027; 1ve 3; Mismatches 0; Indels
                                                                                           Thermomyces lanuginosus; CBS 224.63
                                                                                                                                             1. .18
/label= Sig_peptide
                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 36-38; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS23436 standard; protein; 500 AA.
                                                                                                                                                                                                                                                        95WO-EP002607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacterial polypeptide #12469.
                                                                                                                                                                                                                                                                                        94GB-00013419
(first entry)
                                                                                                                                                                                                                                                                                                                                                      Michelsen B, Rasmussen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYHGYWQKDLYSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-087673/09.
                                                                                                                                                                                                                                                                                                                      (DANI-) DANISCO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT10562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003233675-A1
                              Alpha-amylase
                                                                                                                                                                                                                                                                                      04-JUL-1994;
                                                                                                                                                                                       WO9601323-A1
03-APR-1996
                                                                                                                                                                                                                                                        03-JUL-1995;
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                                                                                                                                                                                                                         18-JAN-1996
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                                                                                                                                          Peptide
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TTTXSXXXXXX
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                                                                                                                                                                                                                                                                                                                                                              Alpha-amylase; thermostable enzyme; baking; Thermomyces lanuginosus; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermophilic alpha-amylase with activity range of 60-80 degrees C -derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs and bakery prods. esp. bread.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fragments (AAR88213-14) of Thermomyces lanuginosus thermostable alpha-amylase (AAR88212) are the products of DNA fragments (AAT10565-66) generated from T. lanuginosus genomic DNA by PCR using primers based on conserved regions of alpha-amylase genes. (Updated on 16-OCT-2003 to standardise OS field)
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                    Score 70; DB 6; Length 494;
Pred. No. 0.019;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69; DB 2; Length 55;
Pred. No. 0.0027;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Thermomyces lanuginosus; CBS 223.63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 40; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                  AAR88213 standard; peptide; 55 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR88212 standard; protein; 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
                                      89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94GB-00013419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.5%;
76.9%;
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rasmussen P;
                                                                                                    1 AYHGYWQQDIYSL 13
                                                     Local Similarity 84.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                               Alpha-amylase fragment
                                                                                                                                                                                                                                                                                 (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-087673/09.
N-PSDB; AAT10565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DANI-) DANISCO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 10; Conserv
        Sequence 494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michelsen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9601323-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-1996.
                                                                                                                                                                                                                                                                              16-OCT-2003
03-APR-1996
                                                                                                                                                                                                                                                AAR88213;
                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches

ઠે 8 AAR88212

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Gaps

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to promote for expression of a polynucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a crop plant such as maize or soybean. The method of producing a transformed plant cauch as maize or soybean. The method of producing a plant with the secombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with the recombinant DNA construct is useful for improving plants with construct is useful for producing plants with conserance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth rate by modification or producing improved plant growth and development under at least on stress condition, improved lightin production or improved galactomannan condition, improved lightin producing or a bacterial polypeptide used in the grown part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic cornar from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                   Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69; DB 8;
Pred. No. 0.027;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 12469; 122pp; English
                                                                                                                                                                                                                                                     Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN19570 standard; protein; 513 AA.
                                                                                                                                                                                                                                                     Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.5%;
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                                       20-FEB-2003; 2003US-00369493
                                                                               21-FEB-2002; 2002US-0360039P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 84.6
                                                                                                                         CAO Y.
HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                               WPI; 2004-061375/06.
                                                                                                                                                                                                           GOLDMAN B S
                                                                                                                                                                                                                                                   Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 500 AA;
                                                                                                                                                                                            CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-2004
18-DEC-2003
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                                                                                                                                                                   (SLAT/)
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8
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The invention relates to a recombinant bush constituct comprising a promoter in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymotlocide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant where the recombinant DNA construct and growing the transformed plant where the recombinant DNA construct is useful for producing plants with the polymotlectide or polypeptide is useful for producing plants with the improved plant properties. e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cold cold in the cold cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or providing improved plant growth and development under at least one stress content, improved lighth production or improved galactomannan content improved lighth production or improved galactomannan contition, mater of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a recombinant DNA construct comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
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Pred. No. 0.057;
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                                                                                                                                                                                                                                                                                                                                                                                           Goldman BS;
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                                                                                                                                                                                                                                                                                                                                                                                             Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2223; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                             Hinkle GJ, Slater SC,
                                                                                                                                                                                        20-FEB-2003; 2003US-00369493.
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HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                       GOLDMAN B S.
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                                                                                                          US2003233675-A1
                                                                                                                                                                                                                                                                                                                                       CHEN X.
                                                                                                                                                    18-DEC-2003.
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                                                                       Bacteria.
                                                                                                                                                                                                                                                                                                                                    (CHEN/)
(GOLD/)
                                                                                                                                                                                                                                                                          CAOY/)
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                                                                                                                                                                                                                                                                                             HINK/)
                                                                                                                                                                                                                                                                                                                    SLAT/)
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A;Cross-references: UNIPROT:Q02905
C;Function:
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hypothetical prote
hypothetical prote
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aspartokinase I-ho
                                                                                                                                               November 7, 2005, 18:40:32; Search time 0.810811 Seconds (without alignments) 830.671 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283416
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                     US-10-820-200-2_COPY_161_167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
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A48305
ALAS3
ALAS3
JC0663
JC06
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B85480
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Gapop 10.0 , Gapext 0.5
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AC0502
T17658
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Maximum DB seq length: 200000000
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Match Length DB
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499
499
624
130
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601
11131
4351
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1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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	RESULT 1 JK0201 alpha-amylase	аве (ЕС	ຄ	.2.1.	.1.1) -	Ası	ber .	Aspergillus ory:	oryzae					•	·	٠,	
	N;Alternate names: glycogenase; C;Species: Aspergillus oryzae C;Date: 31-Mar-1991 #sequence_re	Asper Asper	991	gryc lus c #sec	ogena oryza: quenci	. 1 9 9 9	Ta. evie	s; Taka-amylase A _revision 31-Mar-19	ise A -Mar-1991		#text_change		09-Jul-2004	-2004			
	C; Accession: JK0201 R; Toda, H.; Kondo, Proc. Jpn. Acad. 58 A: Title: The comple	n: JKO; ; Kondc Acad.	201 2, 1 581 581	K.; }	Warit 08-21	2, 1	7. 198:	2 amence	of Taka-	Taka-amvlase	4 4						
	A; Reference A; Molecule	n: JKO;	201 Pr(	JKO:	201		i I										
·	A; KeBidues: 1-478 <10D3 A; Cross-references: UNIPROT: P10529 C; Comment: One atom of calcium per molecule is e C; Comment: This enzyme is a glycoprotein. C; Comment: See also PIR:JT0466 and PIR:JS0240.	ference One at This (	98: 103 180	of of PIR.	PROT:	P10!	529 per copi	molecul rotein. PIR:JS0	e is ess )240.	essential	for	the	activity	.ty.			
	C: Function A; Descript: A; Pathway:	: ion: ca qlycod	ata. ren,	lyze: /sta:	the ch de	hyc	dro.	lysis of	interna	1,4	-alpha	1-D-g]	lucosi	dic b	bonda		
	C, Superfamily: Aspergillus alpha-amylase, alpha-amylase core homology C, Scywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation C; Reywords: glycoprotein; glycosidase core homology <amy> F;133-300/Domain: alpha-amylase core homology <amy> F;197/Binding site: carbohydrate (Asn) (covalent) #status experimental F;210,230,297/Active site: His, Glu, Asp #status experimental</amy></amy>	ily: Ai : glycc Domain ing sit 297/Act	Spe:	rgill oteir lpha- cark	lus a t gl; amyl; oohyd	1phi ycog rate is,	aide Side CO	mylase; ase; hyd re homol asn) (cc	alpha-an Irolase; logy <am) vvalent) status e</am) 	nylase polys ?> #stat	core acchar us exp	homol ride c perime	logy degrac antal	lation	_		
	Query Match Best Local Matches	tch al Simj 7;	Cor	rity nser	Similarity 100 7; Conservative	100.0%; 100.0%; ive	0	Score 4 Pred. N ; Misma	ore 40; DB 2 ed. No. 1.4; Mismatches	2; Le	Length 47 Indels	 8	0; Ga	Gaps	0;		
	8 &	1 SSC 	SSQDYFH          SSQDYFH	FH 7 	1.1												
	RESULT 2 A48305 alpha-amyle C;Species: C;Date: 03.	Asperg	3 31113 994	.2.1. lus s #sec	.1) A Iwamoj	ring.	ecul	rsor - A sion 03-	- Aspergillus awa 03-Feb-1994 #text	us aw	awamori :ext_chan	ge 09	mori change 09-Jul-2004	2004			
	C;Accession: A48305 R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C Curr. Genet. 17, 203-212, 1990 A;Title: Cloning, characterization, and exp	n: A48; D.R.; I E. 17, Loning,	305 38Y	liss, 3-21; harac	F.T 2, 19	o, F 290 zati	Barı ion,	and ex	C.C.; Carmona, C.I expression of two	nona,	C.L.;	Kodama, pha-amyl	ı.; Kodama, K.I alpha-amylase	K.H.; R	l.; Royer, ? genes from	, T.J	r.J.; Aspe
	A;Reference number: A;Accession: A48305 A;Status: preliminary	e number: A48305 n: A48305 preliminary; not	er: 305 Ina)	A48:	305; l	MUID: 902 compared	D:9	3254827; 1 with c	; PMID:2340591 conceptual translation	140591 11 tra	nslati	o u					
	A; Molecule t A; Residues:	type: D : 1-498	Z ⊽ .	AKOR>	i	Š											

Gaps

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A Pathway: glycogen/franch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polys
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polys
F;12-149/Domain: signal sequence #status predicted <SIG>
F;194-321/Domain: alpha-amylase 1 #status experimental <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;195-59;171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,211/Binding site: calcium (Asn) (covalent) #status experimental
F;277,251,318/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon c
A,Reference number: S04548; MUID:89237897; PMID:2785629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922|
A;Accession: A33215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: translation not shown
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-499 <MIZ.>
A;Stesidues: 1-499 <MIZ.>
A;Cross-references: GB:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
B;Genes, M.J.; Dove, M.J.; Seligy, V.L.
R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: A44713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A percipition: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Pathway; glycogen/starch degradation
A; Pathway; glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase; predicted *SIG>
F;1-21/Domain: alpha-amylase 3 #status experimental *MAT>
F;22-499/Product: alpha-amylase 3 #status experimental *MAT>
F;194-321/Domain: alpha-amylase core homology *AMY>
F;194-321/Domain: alpha-amylase core homology *AMY>
F;194-3131,96,231/Binding site: calclum (Asn, Glu, Asp, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;219,318/Active site: His, Glu, Asp #status experimental
                A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N'Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A C;Species: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S04549; A33215; A44713
R;MIrsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: DNA
A, Residues: 1-499 <GEN>
A, Note: the authors refer to this as isozyme I
A, Note: the authors refer to this as isozyme I
R, Mateuura, Y: Kusunoki, M: Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A, Title: Structure and possible catalytic residues of Taka-amylase A.
A, Reference number: A37454; WID: 64212370; PMID: 6669921
A, Contents: annotation; X-ray crystallography, 3.0 angstroms
C; Comment: One atom of calcium per molecule is essential for activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 40; DB 1; Length 499;
100.0%; Pred. No. 1.5;
rative 0; Mismatches 0; Indels
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Pred. No. 1.5;
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A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-499 <WIR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Addissemylaee (EC 3.2.1.1) I precursor [validated] - Aspergillus oryzae Addis anylaes (EC 3.2.1.1) I precursor [validated] - Aspergillus oryzae Addis anylaes (EC 3.2.1.1) I precursor [validated] - Aspergillus oryzae anylaes A Chacesion: Sociata Anizot. 2019 (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (1900) (19
            the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bo A;Bethway: glycogen/etarch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Superfamily: Aspergillus alpha-amylase; hydrolase; polysaccharide degradation
C;Keywords: glycoprofein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>
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                                                                                                                                                                                                                                                    Length 498;
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                                                                                                                                                                                                                                            100.0%; Score 40; DB 2;
100.0%; Pred. No. 1.5;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 7; Conservative
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C;Accession: UN0588
R;Tsukagoshi, N; Furukawa, M; Nagaba, H; Kirita, N; Tsuboi, A; Udaka, S.
R;Tsukagoshi, N; Furukawa, M; Nagaba, H; Kirita, N; Tsuboi, A; Udaka, S.
Gene 84, 119-127; 1989
A;Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for m
A;Reference number: UN0588; MUID:90128276; PMID:2612911
A;Accession: UN0588
A;Residues: 1-499 < TSUP.
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C;Date: 03.Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: B46305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe
A;Reference number: A48305; MUID:90254827; PMID:2340591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A, Pathway: glycogen/starch degradation
A, Pathway: glycogen/starch degradation
C, Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C, Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>F;1-24/Pomain: alpha-amylase #status predicted <MAT>F;194-321/Domain: alpha-amylase core homology <AMY>F;194-321/Domain: alpha-amylase core homology <AMY>F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
A;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Superfamily: Aspergillus alpha-amylase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>
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                                                                                                                                                                                                                                      alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae N;Alternate names: Taka-amylase A C;Species: Aspergillus oryzae C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q96TH4
C;Comment: The alpha amylases are encoded by multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
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Matches 7; Conservative
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                                                                    162 SSQDYFH 168
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R; Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Bioscin: Biochem. Biochem. 56, 174-179, 1992
A; Title: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expression A; Reference number: USO663; MUD:92323146; PMID:1368777
A; Accession: USO663; MUD:92323146; PMID:1368777
A; Accession: USO663; MUD:92323146; PMID:1368777
A; Residues: 1-499 cSHI>
C; Function:
A; Residues: 1-499 cSHI>
C; Function:
A; Poscription: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; hydrolase; polyaaccharide degradation
C; Superfamily: Aspergillus alpha-amylase; bydroclase; polyaaccharide degradation
F; 1-21/Domain: signal sequence #status predicted cAIP>
F; 21-499/Product: alpha-amylase core homology cAMY>
F; 184-321/Domain: alpha-amylase core homology cAMY>
F; 188-binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cydrocession: JT0466
RyTada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
AyTitle: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergill
A;Reference number: JT0466
A;Accession: JT0466
A;Molecule type: DNA
A;Residues: 1-499 cTAD>
A;Cross-references: UNIPROT:P10529
C;Comment: See also PR:JX021 and PR:JX0240.
C;Comment: See also PR:JX021 and molecule is essential for activity.
C;Comment: See also PR:JX021 and molecule is essential for activity.
C;Comment: See also PR:JX021 and molecule is essential for activity.
C;Comment: See also PR:JX021 and molecule is essential for activity.
C;Comment: See also PR:JX021 and molecule is essential for activity.
C;Comment: See also PR:JX021 and molecule is essential for activity.
C;Comment: See also PR:JX021 and molecule is essential for activity.
C;Comment: See also PR:JX11; 275/2; 324/2; 404/3
C;Comment: See also PR:JX121/1; 275/2; 324/2; 404/3
C;Comment: See also PR:JX121/2 as the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pethway: glycogen/fearch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
C;Superfamily: Aspergillus alpha-amylase setting predicted core
C;Comment: alpha-amylase core homology cander
F;124-321/Domain: alpha-amylase core homology cander
F;134-321/Domain: alpha-amylase core homology cander
F;134-321/Domain: alpha-amylase core homology cander
F;134-321,318/Active site: His, Glu, Asp #status predicted
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                                                                                                                                                                                                                                                                                                                     Alternate names: glycogenase; Taka-amylase A
Species: Aspergillus oryzae
Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
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   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 2; Length 499; 100.0%; Pred. No. 1.5;
   Indels
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Best Local Similarity 100.v
Local 7; Conservative
7; Conservative
                                                                                                                                     162 SSQDYFH 168
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                                                                    1 SSQDYFH 7
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Matches
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Tue Nov

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A;Variety: strain Jī
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41943
R;Nicholas, J.
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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NSKDYFH 459
                                                                 38 SSADYFH 44
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SSQDYFH 7
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C;Date: 15-Oct-1999
C;Accession: T18787
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                                                                                                                                                                                 Nyconcains: alpha-acktrin and anoi-1, e-alpha-giucosidase (EC 3.2.1.41)

Nyconcains: alpha-acktrin and anoi-1, e-alpha-giucosidase (EC 3.2.1.41)

C;Species: Lipomyces kononenkoae

C;Species: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004

C;Accession: 07610; PC4116

R;Steyn, A.J.C; Marmur, J.; Pretorius, I.S.

Gene 166, 65-71, 1995

A;Reference number: JC4510; MUD:96105202; PMID:8529895

A;Reference number: JC4510; MUD:96105202; PMID:8529895

A;Reference number: JC4510; MUD:96105202; PMID:8529895

A;Residues: J-624 < 6712-

A;Residues: 1-624 < 6712-

A;Residues: 19-44 < 672-

A;Residues: 29-44 < 672-

A;Residues: 
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C; Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C; Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C; Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F; 1-28/Domain: signal sequence #status predicted <ATG>
F; 48-141/Domain: alpha-amylase starch-binding domain homology <ABD>
F; 320-447/Domain: alpha-amylase core homology <AMY>
F; 320-447/Domain: alpha-amylase core homology <AMY>
F; 344/Finding site: carbohydrate (Asn) (covalent) #status predicted
F; 334, 344/Active site: His, Glu, Asp #status predicted
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C. Species: Arabidopsis thaliana (mouse-ear cress)

C. Species: Arabidopsis thaliana (mouse-ear cress)

C. Species: Arabidopsis thaliana (mouse-ear cress)

C. Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C. Accession: H71415

R. Bevan, M.; Bandroff, I.; Bent, B.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998

A. Authors: Meller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans A.; Fitle: Analysis of I.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A; Reference number: A71400; MUID:98121113; PMID:9461215

A. Reference number: A71415

A. Status: preliminary; nucleic acid sequence not shown; translation not shown
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A,Reaidues: 1-130 <BEV>
A,Cross-references: UNIPROT:023373; GB:297338; NID:92244870; PID:e326912; PID:92244877
C,Genetics:
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                                                                     illulanase (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae) Alternate names: LKA1 protein; raw starch-degrading amylase (Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 40; DB 1; Length 624; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 7; Conservative 0; Mismatches 0; Indels
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Pred. No. 6.1;
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Best Local Similarity 85.7%;
Matches 6; Conservative
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A,Cross-references: UNIPROT:039309; EMBL:AF030027; NID:g2605950; PIDN:AAC59593.1; PID:g2.
A;Experimental source: strain NS80567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosidues: 1-601 - MIL.
A;Kosidues: 1-601 - MIL.
A;Cross-references: UNIPROT:017552; EMBL:293372; PIDN:CAB07545.1; GSPDB:GN00021; CESP:BE
A;Experimental source: clone BE10
envelope protein - equine herpesvirus 4 (strain NS80567)
C;Species: equine herpesvirus 4
A;Variety: strain NS80567
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42616
R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998
A;Title: The DNA sequence of equine herpesvirus-4.
A;Fitle: The DNA sequence of equine herpesvirus-603335
A;Accession: T42616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein BE10.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 36;
1; Mismatches 0; Indels
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C;Species: human herpesvirus 7
                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: pseudorabies virus glycoprotein gp63
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Pred. No. 53;
2; Mismatches
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A,Introns: 21/3; 54/3; 117/2; 157/1; 212/2; 533/3
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Mismatches

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Search completed: November 7, 2005, 18:58:46 Job time: 1.81081 secs
            5; Conservative
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82 QDYFH 86
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R. Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A.;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9633030
A;Reference number: Z14126; MUID:98360089; PMID:9633030
A;Reference: Preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-4351 «NAK»
A;Residues: 1-4351 «NAK»
A;Residues: 1-4351 «NAK»
A;Residues: UNIPROT:088277; EMBL:AB011527; NID:93449285; PIDN:BAA32458.1; PID:93
A;Gene: MEGFI
C;Superfamily: rat MEGFI protein; cadherin repeat homology; EGF homology; laminin G repe
F;3738-3949/Domain: EGF homology «EGF»
F;3992-4023/Domain: EGF homology «EGF»
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C;Species: Armadillidium vulgare (common pill bug)
C;Species: Armadillidium vulgare (common pill bug)
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: JC7121
R;Okuno, A.; Hasegawa, Y.; Ohira, T.; Katakura, Y.; Nagasawa, H.
R;Okuno, A.; Hasegawa, Y.; Ohira, T.; Katakura, Y.; Nagasawa, H.
A;Title: Characterization and cDNA cloning of androgenic gland hormone of the terrestria
A;Reference number: JC7121; MUID:20001935; PMID:10529379
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A;Status: preliminary
A;Molecule: mRNA
A;Residues: 1-144 <0KU>
A;Cross-references: UNIPROT:Q9U8R2; DDBJ;AB029615; GB:AB029615; NID:g6446571; PID:g64465
A;Experimental source: androgenic gland
submitted to the EMBL Data Library, December 1995
A;Description: Determination and analysis of the complete nucleotide sequence of human
A;Reference number: Z22022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Rattus norvegicus (Norway rat)
Jate: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004; Accession: T00252
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                                      A, Description: Determination and analysis of the complete nucleot: A, Reference number: Z22022
A, Reference number: Z22022
A, Reference number: Z22022
A, Accession: T41943
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Followile type: DNA
A, Residues: 1-1131 «NIC»
A, Cross-references: UNIPROT: P52339; EMBL: U43400; PIDN: AAC54703.1
C, Genetics: A, Note: U41
C, Superfamily: herpesvirus DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.5%; Score 33; DB 2; Length 4351; 71.4%; Pred. No. 4.6e+02; ive 1; Mismatches 1; Indels
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Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
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Matches 5; Conservative
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943 ASRDYFH 949
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Best Local Similarity
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LENGTH: 476
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                                                                                                          7, 2005, 18:58:04; Search time 6.95174 Seconds. (without alignments) 782.441 Million cell updates/sec
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Sequence 10,
Sequence 22,
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Sequence 30,
Sequence 18,
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| Cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.ppp:*
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| Cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.ppp:*
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| Cgn2_6/ptodata1/pubpaa/US00_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/US00_NEW_PUB.ppp:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-184-771-10
US-10-186-042-7
US-10-644-187-7
US-10-926-720-10
US-11-064-196-10
US-11-064-196-10
US-10-815-495-22
US-10-815-495-30
US-10-815-495-30
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                                                                             OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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597, App
22723, A
12469, A
2223, Ap
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Publication No. US20050054071A1

GENERAL INPORMATION:
APPLICANT: Talra, Hiroaki
APPLICANT: Tragi, Shinobu
APPLICANT: Allain, Eric
APPLICANT: Hjort, Carsten
APPLICANT: JUKso-Nielsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490,500-US
CURRENT APPLICATION NUMBER: US/10/877,849
CURRENT FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
US-10-797-393A-5
US-10-877-849-40
US-10-877-849-40
US-10-218-990-42
US-10-218-990-42
US-10-486-868-13
US-10-486-868-13
US-10-877-849-8
US-10-877-849-8
US-10-877-849-8
US-10-877-849-8
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US-10-369-493-52639
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US-10-425-115-239140
US-10-425-115-239140
US-10-486-868-18
US-10-486-868-18
US-10-732-923-7480
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100.0%; Pred. No. 1.1e-06;
ive 0; Mismatches 0;
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ORGANISM: Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AYHGYWQQDIYSL 13
  FEATURE:
NAME/KEY: mat_peptide
LOCATION: (1)..(476)
US-10-877-849-43
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1 AYHGYWQQDIYSL 13
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Best Local Similarity
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                  Sequence 10, Application US/10184771
FUDDICATION NO. US20030170769A1
GENERAL INFORMATION:
APPLICANT: Svendeen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
ITILE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Biggard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796,204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28
FRIOR APPLICATION NUMBER: US/09/672,459
FRIOR FILING DATE: 1998-10-29
FRIOR FILING DATE: 1998-10-29
FRIOR FILING DATE: 1996-04-30
FRIOR APPLICATION NUMBER: 0515/96
FRIOR APPLICATION NUMBER: 0712/96
FRIOR APPLICATION NUMBER: 0715/96
FRIOR FILING DATE: 1996-06-28
FRIOR FILING DATE: 1996-07-11
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Publication No. US20301171236A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
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; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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Best Local Similarity
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CORGANISM: A. Oryzae
US-10-184-771-10
-10-184-771-10
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US-10-186-042-7
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US-10-815-495-22

Sequence 22, Application US/10815495

Publication No. US20040191864A1

GENERAL INFORMATION:
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Mutants Of Aspergillus Niger
FILE REFERENCE: 10345.200-US
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.2
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APPLICANT: Bedersen, Sven
APPLICANT: Pedersen, Sven
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
FILE REFERENCE: 5835.200-US
CURRENT APPLICATION NUMBER: US/10/820,200
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US/09/710,339
PRIOR APPLICATION NUMBER: US 60/165,786
PRIOR APPLICATION NUMBER: US 60/165,786
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VETSION 3.2
SSEQ ID NO 2
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100.0%; Pred. No. 1.1e-06;
vative 0; Mismatches 0;
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100.0%; Score 13; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0;
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/11/064,196
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR PILING DATE: 2000-08-10
PRIOR PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10820200 Publication No. US20040229764A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Aspergillus niger
US-10-815-495-22
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Best Local Similarity 100.0
Matches 13; Conservative
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US-11-064-196-10
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LENGTH: 498
TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
     REFERENCE/DOCKET NUMBER: 4394.204-US
                                                                 INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TYPE: class
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
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PRIOR APPLICATION NUMBER: 2004-11-03
PRIOR PILING DATE: 2000-09-28
PRIOR PILING DATE: 2000-09-28
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-06-28
PRIOR PILING DATE: 1996-01-11
PRIOR PILING DATE: 1996-01-11
PRIOR PILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/10980759; Publication No. US20050118695A1; GENERAL INFORMATION: APPLICANT: Svendsen, Allan; APPLICANT: Borchert, Torben APPLICANT: Bisgard-Frantzen, Henrik TITLE OF INVENTION: Alpha-Amylase Mutants; PILE REPERRICE: 4736.204-US; CURRENT APPLICATION NUMBER: US/10/980,759; CURRENT FILING DATE: 2004-11-03
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Publication No. US20050170487A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Bacillus licheniformis US-10-980-759-7
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US-11-064-196-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Traira, Rikako
APPLICANT: Traira, Rikako
APPLICANT: Allain, Eric
APPLICANT: Hjort, Carsten
APPLICANT: Hjort, Carsten
APPLICANT: Vikso-Nielsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490.500-US
CURRENT FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE PATENTING DATE: 2004-06-25
SEQ ID NO 40
LENGTH: 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Olsen, Hans Sejr
APPLICANT: Pedersen, Sven
APPLICANT: Pedersen, Sven
TILLGANT: Festersen, Rikke Monica
TILLGANT: Festersen, Rikke Monica
TILLB OF INVENTION: ALCOHOL PRODUCT PROCESSES
FILE REPERENCE: 10391.200-US
CURRENT APPLICATION NUMBER: US/10/797,393A
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
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                                                                                                  Sequence 5, Application US/10797393A; Publication No. US20040219649A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Aspergillus oryzae
  99 AYHGYWQQDIYSL 111
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ORGANISM: Artificial
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Matches 13; Conserv
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US-10-877-849-40
                                                            RESULT 12
US-10-797-393A-5
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Sequence 18, Application US/10815495

Publication No. US20040191864A1

GENERAL INFORMATION:

APPLICANT: Novozymes Biotech, Inc.

APPLICANT: Brody, Howard

TITLE OF INVENTION: Mutants Of Aspergillus Niger

TITLE OF INVENTION: Mutants Of Aspergillus Niger

TITLE OF INVENTION: NUMBER: US/10/815,495

CURRENT PILING DATE: 2004-03-31

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.2

SEQ ID NO 18

LENGTH: 499
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                                                                                                  Score 13; DB 16; Length 498;
Pred. No. 1.2e-06;
; Mismatches 0; Indels
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100.0%; Score 13; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                             Sequence 30, Application US/10877849
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION;
; APPLICANT: Taira, Rikako
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Hjort, Carsten
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; TITLE OF INVENTION: HYBRID ENZYMES
; TITLE OF INVENTION: HYBRID ENZYMES
; TITLE OF INVENTION: HYBRID ENZYMES
; TITLE OF SEQ ID NOS: 43
; CURRENT APPLICATION WOBBR: US/10/877,849
; NUMBER: OF SEQ ID NOS: 43
; SEQ ID NO 30
; LENGTH: 498
; TURNENT: HAS
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Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                             0; Mismatches
                                                                                                  100.08;
               TYPE: PRT; ORGANISM: Aspergillus Oryzae US-10-820-200-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30
                                                                                                                                                                                                            98 AYHGYWQQDIYSL 110
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CRGANISM: Aspergillus niger
US-10-815-495-18
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                                                                                            Query Match
Best Local Similarity 100.0
Matches 13, Conservative
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US-10-877-849-30
LENGTH: 498
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US-10-228-063-45
i Sequence 45, Application US/10228063
; Sequence 45, Application US/10228063
; Publication No. US2003013585A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 10946.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT PILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PSELSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 13; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels (
APPLICANT: Tkagi, Shinobu
APPLICANT: Allain, Eric
APPLICANT: Hjort, Carten
APPLICANT: Hjort, Carten
APPLICANT: Vikso-Nielsen, Anders .
TITLE OP INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REPERENCE: 10490.500-US
CURRENT APPLICATION NUMBER: US/10/877,849
CURRENT APPLICATION NUMBER: US/10/877,849
CURRENT PILING DATE: 2004-06-25
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: PATENTING DATE: DENGTH: GOOGANISM: ATTIFICIAL
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; OTHER INFORMATION: Artificial
US-10-877-849-36
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Sequence 10, Appl
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Sequence 10, Appl
Sequence 11, Appli
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Sequence 11, Appl
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Sequence 12, Appl
Sequence 12, Appl
Sequence 234, Appl
Sequence 234, App
Sequence 234, App
Sequence 234, App
Sequence 234, Appl
Sequence 2, Appl
Sequence 2, Appl
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Sequence 7, Appli
Sequence 7, Appli
                                                                                                  November 7, 2005, 18:45:18; Search time 1.95753 Seconds (without alignments) 495.746 Million cell updates/sec
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Sequence 7, Al
Sequence 10,
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Sequence 70,
Sequence 73,
Sequence 63,
Sequence 63,
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-248-766A-18703
US-09-108-857-2
US-08-947-965-74
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US-09-182-838A-10
US-09-182-859-7
US-09-672-459-7
US-09-636-252A-10
US-08-204-656B-11
US-08-204-656B-11
US-08-470-702-11
US-08-470-702-11
US-08-467-831-12
US-08-467-831-12
US-08-467-831-12
US-08-467-831-34
US-08-467-831-34
US-08-467-831-34
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US-08-477-346-63
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13
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                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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28 6 46.2 713 3 10.06.471036-63 Sequence 63, Appl 20 6 46.2 713 3 10.06.471036-63 Sequence 63, Appl 20 6 46.2 713 4 10.06.471026-63 Sequence 63, Appl 20 6 46.2 713 4 10.00.04.452 Sequence 73, Appl 20 6 46.2 713 4 10.00.04.452 Sequence 73, Appl 20 6 46.2 713 4 10.00.04.452 Sequence 73, Appl 20 6 46.2 1938 10.00.44.65 Sequence 73, Appl 20 6 46.2 1938 10.00.04.452 Sequence 73, Appl 20 6 46.2 1938 10.00.04.452 Sequence 73, Appl 20 6 46.2 1938 10.00.04.452 Sequence 73, Appl 20 6 40.00.00.452 Sequence 73, Appl 20 6 40.00.452 Sequen
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TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
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// TOPOLOGY: linear

US-08-343-804-7
                                                                                  New York
                                                                                                           USA
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                                                                            STATE: N
COUNTRY:
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                                                                                                                                                                                                                                                         APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUNTRY: USA

ZIP: 10174-6401

COMPUTER READBLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATEMIL Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,610

FILING DATE: 02-JUN-1995

CLASSIFICATION 1435

PRIOR APPLICATION NUMBER: US/08/343,804

FILING BAPLICATION NUMBER: US/08/343,804

FILING APPLICATION NUMBER: US/08/343,804

FILING APPLICATION NUMBER: US/08/343,804
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APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bordeer, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  Sequence 7, Application US/08459610
Patent No. 5801043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lowney Dr., Karen A.
REGISTATION UNDBER: 31,274
REPERENCE/DOCKET NUMBER: 4054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-876-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 animo acids
TYPE: amino acid
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Patent No. 5830837
                               78 AYHGYWQQDIYSL 90
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                  RESULT 2
US-08-459-610-7
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ADDRESSEE: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: No. 59891690 No. 5989169disk of No. 5989169th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York STATE: New York COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                  COMPUTE: USA

ZIP: 1014-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,804

FILING DATE: 22-NOV-1994

CLASSIFICATION: 435
ATONREY/AGENT INPORMATION:
NAME: LOWING DY., KAYER A.
REGISTRATION NUMBER: 31,274

REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-867-0123
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPUTER: TBM TOWN TOWNER: TBM TOWN TOWNER: TBM TOWN TOWNER: TBM TOWN TOWNER: TBM TOWNER: TB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08; Fr.
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 478 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AYHGYWQQDIYSL 13
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Matches 13; Conservative
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Sequence 7, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TILLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERRNCE: 4796.204-03
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 0515/96
EARLIER APPLICATION NUMBER: 0712/96
EARLIER APPLICATION NUMBER: 0712/96
EARLIER APPLICATION NUMBER: 0712/96
EARLIER APPLICATION NUMBER: 0715/96
EARLIER APPLICATION NUMBER: 0715/96
EARLIER APPLICATION NUMBER: 1263/96
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AYHGYWQQDIYSL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-672-459-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Patent No. 6022724

GENERAL INFORMATION:

APPLICANT: Bisg rd-Frantzen, Henrik

APPLICANT: New York

STREET: 405 Lexington Avenue, 64th Floor

COUNTRY: New York

STATE: New York

STATE: New York

COUNTRY: United States of America

STATE: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                   Query Match 100.0%; Score 13; DB 2; Length 478; Best Local Similarity 100.0%; Pred. No. 4.7e-07; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 13; DB 3; Length 478; 100.0%; Pred. No. 4.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REGISTRATION NUMBER: 4394.204-US
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECAX: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-867-0123
TELEFAX: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FLILING DATE: 13.FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/683,8381
                           LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-600-908A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 478 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                          78 AYHGYWQQDIYSL 90
                                                                                                                                                                                                                                                                                                                            1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 AYHGYWQQDIYSL 90
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Best Local Similarity 100.
Matches 13, Conservative
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     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-683-838A-10
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Gaps

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100.0%; Score 13; DB 3; Length 478; 100.0%; Pred. No. 4.7e-07; Live 0; Mismatches 0; Indels

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                                                                                                                                                                                              Query Match 100.0%; Score 13; DB 4; Length 478; Best Local Similarity 100.0%; Pred. No. 4.7e-07; Matches 13; Conservative 0; Mismatches 0; Indels
ORGANISM: Bacillus licheniformis
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RESULT 6 US-09-182-859-7

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RESULT 11
US-08-204-656B-12
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VG-09-656-252A-10

JG-09-656-252A-10

Sequence 10, Application US/09636252A

Patent No. 6440716

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Biggard-Frantzen, Henrik

APPLICANT: Borchert, Torben Vedel

TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 0776/JF216-US2

CURRENT APPLICATION NUMBER: US/09/636,252A

CURRENT APPLICATION NUMBER: US/09/636,252A

CURRENT APPLICATION NUMBER: US/09/636,252A

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 10

LENGTHARE: FastSEQ for Windows Version 3.0

LENGTHA 478
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Sequence 7, Application US/10186042

Patent No. 6642044

GRNERAL INFORMATION:

APPLICANT: Svendeen, Allan

APPLICANT: Borchert, Torben

APPLICANT: Balsgard-Frantzen, Henrik

TILLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 4796.204-US

CURRENT APPLICATION NUMBER: US/10/186,042

CURRENT APPLICATION NUMBER: US/09/672,459

PRIOR APPLICATION NUMBER: 09/182,859

PRIOR FILING DATE: 1900-09-28

PRIOR FILING DATE: 1998-10-29

PRIOR FILING DATE: 1996-04-30

PRIOR APPLICATION NUMBER: 0712/96

PRIOR APPLICATION NUMBER: 0712/96

PRIOR APPLICATION NUMBER: 0712/96

PRIOR APPLICATION NUMBER: 0712/96

PRIOR PILING DATE: 1996-04-30

PRIOR PILING DATE: 1996-07-11

PRIOR APPLICATION NUMBER: 0775/96

PRIOR APPLICATION NUMBER: 0775/96

PRIOR APPLICATION NUMBER: 0775/96

PRIOR PILING DATE: 1996-07-11

PRIOR PILING DATE: 1996-07-11

PRIOR PILING DATE: 1996-07-11

PRIOR PILING DATE: 1996-11-08

NUMBER OF SEQ ID NOS: 37

LENGTH: 478

LENGTH: 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 AYHGYWQQDIYSL 90
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Best Local Similarity 100.
Matches 13; Conservative
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; ORGANISM: A. Oryzae
US-09-636-252A-10
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78 AYHGYWQQDIYSL 90

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                                                                                            APPLICANT: Mateul, Ikuo
APPLICANT: Mateul, Ikuo
APPLICANT: Miyairi, Sachio
APPLICANT: Miyairi, Sachio
APPLICANT: Miyairi, Sachio
APPLICANT: Miyairi, Sachio
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
ONDERSONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08204656B
; Patent No. 553882
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Matsui, Ikuo
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichio
TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CCLASSIF [CATION IN PORMATION:
NAME: Walner: Marc 8.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.2%; Score 6; DB 1;
100.0%; Pred. No. 1.3;
iive 0; Mismatches
Sequence 11, Application US/08204656B; Patent No. 5538882; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYHGYW 12
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RESULT 13

US-08-470-702-12

Squence 12, Application US/08470702

Sacquence 12, Application US/08470703

APPLICANT: MYAZUHY

TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLLASE,

TITLE OF INVENTION: VARIANT-TON-TYPE CARBOHYDRATE HYDROLLASE,

TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE,

TITLE OF INVENTION: VARIANT-TYPE CARBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US/08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, WARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6; DB 1;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
   APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REPERENCE/DOCKET NUMBER: 234-252P
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
meter Ax: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; P. Matches 6; Conservative 0;
                                                                                                                                                                                                                                                               TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: N-terminal US-08-470-702-11
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AYHGYW 6
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Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TILLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                    COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: THEN PC compatible
COMPUTER: THEN PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATORNEY/AGENT INORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 234-252P
TELESCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703) 205-8050
TELEFRAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
ZIP: 22042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AYHGYW 12
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US-08-470-702-11
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APPLICANT: MATSULIKUO
APPLICANT: MATSULIKUO
APPLICANT: MATSULIKUO
APPLICANT: MATSULIKUO
APPLICANT: MITAIRI, SACHIO
APPLICANT: MANDAN, MOLICHAI
TITLE OF INVENTION: VARIANT-TYPE CARBCHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT-TYPE CARBCHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT-TYPE CARBCHYDRATE
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: BILD Gatehouse Road, Suite 500 East
CONNETRY: U.S.A.
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STRATE: Virginia
COMMUTRY: U.S.A.

ZITP: 22042
COMPUTRY: U.S.A.
ZITP: 22042
COMPUTRY: BEACHION RAIS
COMPUTRY: U.S.A.
ADPLICATION NUMBER: US/08/467,831
FILING DATE: OC-OMBATION
APPLICATION NUMBER: 31.81
FILING DATE: OC-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC 3.181
REPERENCE/DOCKET NUMBER: 3.182
REPERENCE/DOCKET NUMBER: 3.183
REPERENCE/DOCKET 
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                                                                                                                                                                                                                                                                                                                                             Length 14;
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Best Local Similarity 100.0%; Pred. No. 1.3
Matches 6; Conservative 0; Mismatches
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; Sequence 11, Application US/08467831
; Patent No. 5635378
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
"COOLOGY: linear
"COOLOGY: linear
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                    ANTI-SENSE: NO FRAGMENT TYPE: N-terminal US-08-470-702-12
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Best Local Similarity
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                                                                                                                                                                  Sequence 12, Application US/08467831
| Patent No. 5635378
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: MATSUI, IKUO
| APPLICANT: MIYAIRI, SACHIO
| APPLICANT: HONDA, KOICHI
| TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
| TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
| TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ER COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 8110 Gatchouse Road, Suite 500 East CITY: Falls Church
CITY: Falls Church
CONTEXT: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 7, 2005, 19:00:09 Job time : 2.95753 secs
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REPERBINCE/DOCKET NUMBER: 234-252P
TELECOMFUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.2%; 5cc.
100.0%; Pre/
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; FRAGMENT TYPE: N-terminal
US-08-467-831-12
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INFORMATION FOR EQG ID NO: SEQUENCE GRANACTERICSTICS: LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
5. 6; Conservative
6; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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7 AYHGYW 12
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                                      1 AYHGYW 6
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                       OM protein - protein search, using sw model
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7, 2005, 18:25:16 ; Search time 291.301 Seconds (without alignments) 661.194 Million cell updates/sec US-10-820-200-2 2684 November Run on:

1 MVAWWSLFLYGLQVAAPALA......LPRVLYPTEKLAGSKICSSS 498 Perfect score:

**BLOSUM62** Scoring table: Sequence:

2105692 segs, 386760381 residues Gapop 10.0 , Gapext 0.5 Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqD1990s: geneseqD2000s: geneseqD2001s: geneseqD2002s: geneseqD2003ss: geneseqD2003bs: A\_Geneseq\_16Dec04:\* geneseqp1980s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Aab84206 Amino aci	Adt89628 Aspergill	Adt89632 Aspergill	Aar72450 Aspergill	Aar78270 Aspergill	Aaw14500 Aspergill	Abp96630 Alpha-amy			Abb09072 Aspergill		Ami		Asp	Ads75939 Aspergill	Aar88212 Alpha-amy			Aap81161 Recombina				Aar63185 Variant a	Aar63187 Variant a	Aar63186 Variant a
	αī	AAB84206	ADT89628	ADT89632	AAR72450	AAR78270	AAW14500	ABP96630	AAR46065	AAR79025	ABB09072	ABB80177	ABP97894	ABB80178	AAE24207	ADS75939	AAR88212	AAR07574	AAP81180	AAP81161	AAR24136	AAP70571	AAR63184	AAR63185	AAR63187	AAR63186
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	Length DB	498	499	498	478	478	478	1095	478	478	423	495	494	630	484	484	493	512	511	511	468	494	468	468	468	452
ф	Query Match	100.0	99.6	99.5	95.8	95.8	95.8	95.7	95.1	93.3	80.1	78.2	75.0	68.4	66.2	66.2	62.1	54.0	52.2	52.1	52.0	52.0	51.9		51.7	49.9
	Score	2684	2674	2662	2572	2572	2572	2569	2552	2503.5	2151	2100	2012	1835	1778	1778	1666.5	1449	1400.5	1398.5	1397	1396.5	1392	1391	1387	1338
	Result No.	1	7	e	4	S	9	7	<b>c</b> o	6	10	11	12	13	14	15	16	17	18		20	21	22	23	24	25

555 6 ABB80179 556 6 ABB97896 560 8 ABP97896 549 6 ABP97895 513 8 ADN19570 5513 8 ADN19570 552 6 ABC03092 547 8 ADS30907 713 7 ADC23483 719 4 AAB74220 719 2 AAX31731 719 2 AAX31731 719 2 AAX31621 719 2 AAX31621 719 4 AAB59956 719 4 AAB74216 719 4 AAB74216		ADP97899 Amino aci Ad823436 Bacterial Abn97895 Amino aci		Ads44293 Bacterial Abu03092 Alpha amy	ш,		_	Aar10051 Cyclomalt Aab74219 Bacillus	Aay31731 Bacillus	Aay30621 Amino aci	Aay94271 Bacillus	Aab59956 Bacillus	Aab74216 Bacillue
6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ABB80179 ABP97896	ABP97899 ADS23436 ARP97895	ADN19570 ADS44249	ADS44293 ABU03092	ADS30907	ADS30029 ADC23483	AAB74220	AAR10051 AAB74219	AAY31731	AAY30621	AAY94271	AAB59956	AAB74216
	547 6	500 8	113 8	93 8	347 8	347 8 713 7	119 4	712 719 4	119 2	119 2	119 3	119 4	119 4
	1214.5	1160 1160	1015.5 898.5	873 541	483.5	480.5 456.5	453	452.5 452	450	450	450	450	450
11214.5 11183 1163 1160 1015.5 898.5 898.5 488.5 456.5 450.5 450.6 450 450 450 450 450 450 450 450	26	8 6 C	35	3 3 3 4	35	36	38	39 40	41	42	43	44	45

## ALIGNMENTS

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Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose; alcohol; starch; dough improver; brewing; starch liquification.
                                               Amino acid sequence of a fungamyl-like alpha-amylase.
                                                                                                                                                                       ŝ
                                                                                                                                                                       Pedersen
      AAB84206 standard; protein; 498 AA
                                                                                                                                                                       Svendsen A,
                                                                                                                             10-NOV-2000; 2000WO-DK000626.
                                                                                                                                           99DK-00001617
                                  06-AUG-2001 (first entry)
                                                                                                                                                        (NOVO ) NOVOZYMES AS.
                                                                                                                                                                                    WPI; 2001-367478/38.
N-PSDB; AAF90208.
                                                                                                                                                                       Bisgard-Frantzen H,
                                                                                  Aspergillus oryzae.
                                                                                                WO200134784-A1.
                                                                                                                                           10-NOV-1999;
                                                                                                              17-MAY-2001.
                    AAB84206;
AAB84206
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New variant of Fungamyl-like alpha-amylase, useful for production of malcose syrups, includes mutations that improve stability against heat and acidic pH.

Claim 1; Page 42-45; 49pp; English.

The present sequence represents a fungamyl-like alpha-amylase. The specification describes variants of this fungamyl-like alpha-amylase, which have an alceration in one the amino acid regions 98-110, 150-160, 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or substitution of an amino acid or an insertion of an amino acid downstream of a particular position. The variants retain alpha-amylase activity, and have better heat stability and/or stability at acidic ph, relative to wild-type enzyme. The variants can therefore be used at higher removerse (more efficient conversion or faster reaction, and have reduced need for cooling and reduced risk of contamination). The variants amay also be used in conjunction with other enzymes, particularly gluccoamylase during dextrinisation. The variants are used to produce

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09 9 180

240 240

120 120 180 300 300 360 360 420 420

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or alcohol, from starch; increase fermentability
                                                                                                                                                                                                     MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
                                                                                                                                                                                                                                                VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
                                                                                                                                                                                                                                                                                                                                                                           KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
                                                                                                                                                                                                                                                                                                                                                                                          SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAARIILNDGIPIIYAGQEQHYAGGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
                                                                                                                                                                                   MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
                                                                                                                                                                                                                                TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
                                                                                                                                                                                                                                                                              KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
                                                                                                                                                                                                                                                                                                                            VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
                                                                                                                                                                                                                                                                                                                                                                                                                          SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
                                                                                                                                      Length
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (amyB) protein.
                                                               syrups, particularly of high maltose content, or alcohol
dough improver for baked goods; in brewing, to increase
the wort; and for liquefaction of starch
                                                                                                                                  Score 2684; DB 4;
Pred. No. 3e-226;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amyB; alpha-amylase B; enzyme
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                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 498; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus niger
                                                                                                             Sequence 498 AA;
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The present invention relates to a method of producing heterologous bological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide sequences comprising modification of glucomytase (glash) and recovering heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase B (amyB) protein.
                                            mutant of
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                                      Producing heterologous biological substance comprises culturing mutant owild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
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                                                                                                                                                                                                                                                                                                                                                                        MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADOKYCGG
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                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                Score 2674; DB 8;
Pred. No. 2.3e-225;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus niger neutral alpha-amylase A (amyA)
                                                                                                             18; 58pp; English
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99.6%; Pred
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Best Local Similarity 99.6
Matches 496; Conservative
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                                                                                                             Example 10; SEQ ID NO
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              N-PSDB; ADT89627
                                                                                                                                                                                                                                                                     Sequence 499 AA;
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                                                                                    substance
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                                                                                                                                                                                                                                                                                     Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Bacillus derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance.
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Pred. No. 1.9e-216;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 75-76; 105pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bisgard-Frantzen H,
                                                                                                               AAR72450 standard; protein; 478
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94WO-DK000370
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94DX-00000140.
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Matches 477; Conservative
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                                                                                                                                                                                           (revised)
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                                                                                                                                                                                                                                                                                                                                                 thermostable.
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01-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKAVAAFIILNDGIPIIYAGQEQHYAGGND 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGSOIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2662; DB 8;
Pred. No. 2.6e-224;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; SEQ ID NO 22; 58pp; English.
                                                                                                                                                                                                       (NOVO ) NOVOZYMES BIOTECH INC
                                                                                                                                                                   31-MAR-2003; 2003US-0459902P.
                                                                                                                               31-MAR-2004; 2004US-00815495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 RVLYPTEKLAGSKIC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.24; al Similarity 99.64; 493; Conservative
                                                                                                                                                                                                                                               Brody H;
                                                                                                                                                                                                                                                                                     WPI; 2004-708545/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 493; Conserv
               Aspergillus niger
                                                                                                                                                                                                                                                                                                         N-PSDB; ADT89631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 498 AA;
                                                     US2004191864-A1
                                                                                                                                                                                                                                               Connelly M,
                                                                                           30-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidation stable alpha amylases can be used for the simultaneous desizing and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or Asp. The parent alpha amylase is pref. derived from a Bacillus species, although alpha amylases of fungal origin can also be used. This sequence is the wild type (unmodified) alpha amylase of Aspergillus oryzae
                                                                                                                           420
               FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
                                                                 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                       fabric; starch;
  PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
                                                                                                               LIASANAIRNYAISKOTGFVTYKAMPIYKDDITIAMRKGTDGSQIVTILSNKGASGDSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 simultaneous desizing or starch derivs.
                                                                                                                                                 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS
                                                                                                                                                               LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPWAGGLPRVLYPTEKLAGSKICSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478;
                                                                                                                                                                                                                                                                                                                                  ylase; oxidation; desizing; bleaching; scouring; sable; methionine; Bacillus licheniformis; amyloliquefaciens; Bacillus stearothermophilus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                            Aspergillus oryzae alpha amylase (mature protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2572; DB 2;
Pred. No. 1.9e-216;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of an oxidation stable alpha-amylase - for bleaching or scouring of fabrics contg. starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nilsson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 25-26; 37pp; English.
                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 표,
                                                                                                                                                                                                                                      478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-DK000371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94DK-00000141
                                                                                                                                                                                                                                    AAR78270 standard; protein;
                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.8
Matches 477; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marcher D,
                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-283767/37.
                                                                                                                                                                                                                                                                                                                                                                           oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                      amylase;
                                                                                                                                                                                                                                                                                                                                                thermostable;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-1994;
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                                                                                                                                                                                                                                                                                    17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                          Aspergillus
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 261
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/label= loop 1 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
                           WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
                                                                     200
                                                                                                  NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 180
                                                                                                                                                                                                             320
                                                                                                                                                                                                                                 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
                                                                                                                                                                                                                                                                                  FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
                                                                                                                                                                                                                                                                                                      /note= "at least one amino acid residue of a parent alpha -amylase (used as a template for a variant) corresponding to 7-23 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 8-18 of AAW14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                    LIASANAIRNYAISKDIGFVIYKNWPIYKDDITIAMRKGTDGSQIVTILSNKGASGDSYT 440
                                                                                                                                                                                                                                                                                                                                                                                      LIASANAIRNYAISKÖTGFVTYKOWPIYKODITIAMRKGTÖGSQIVTILSNKGASGDSYT 420
                                                                                                                                                                                                                                                                                                                                                                                                                       LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478
                                                                                                                                                              DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                        DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                                                                                             PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
                                                                     NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-amylase, mature; Bacillus licheniformis; termamyl; fungamyl; Aspergillus oryzae; Bacillus amyloliquefaciens; altered property; calcium dependency; substrate binding; stability; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction; sweetener; ethanol production; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13. .45
/label= loop 1 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae alpha-amylase (mature protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14. .40
/label= loop 1 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment; claim 35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein; 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus oryzae
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Misc-difference
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                                  61
                                                                                                     121
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81
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21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI

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96WO-DK000057
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                                                                        23-OCT-1995;
10-NOV-1995;
                              05-FEB-1996;
   08-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid
                                           66. .84
/label= loop 2 modification region
/note= "at least one amino acid residue of a parent alpha
/mote= "at least one amino acid residue of a parent alpha
-mylase (used as template for a variant) corresponding
to 44-57 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181. .184

/note= "an amino acid fragment corresponding to this region is deleted from the parent sequence of a variant Pungamyl; claim 43"

291. .31

/label= 1009 8 modification region
/note= "at least one amino acid residue of a parent alpha amylase (used as a template for a variant) corresponding to 322-346 of ANM1498 is deleted or replaced with a fragment corresponding to this fragment; claim 36"
                                                                                                                                                                                                                                     98. .210 / Jabel= loop 3 modification region /label= loop 3 modification acid residue of a parent alpha -amylase (used as a template for a variant) corresponding to 117-185 of AAW1499 is deleted or replaced with a fragment corresponding to this fragment; claim 24"
                                                                                                                                                                                                                                                                                                                                               /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 121-181 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165. .177
/label= loop 3 modification region
/label= loop 3 modification acid residue of a parent alpha
/note= wat least one amino acid residue of a parent alpha
-mylase (used as a template for a variant) corresponding
to 195-202 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= loop 8 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 325-345 of AAW14498 is
deleted or replaced with a fragment corresponding to this
fragment; claim 38"
                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= loop 3 modification region
/label= loop 3 modification where at least one amino acid
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 196-198 of AAW14499 is
deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                     121. .181
/note= "at least one amino acid residue of a parent alpha
   deleted
                                                                                                                                                                                            deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-206 of AAW14499; claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                70. 78
/label= loop 2 modification region
/label= loop 2 modification where at least one amino acid
residue of a parent alpha-amylase (used as a template
a variant) corresponding to 48-51 of AAW14499 is delet
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121. 174
/note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template a variant) corresponding to this fragment is deleted oreplaced with a fragment corresponding to 102-199 of AAW14499; claim 42"
corresponding to 14-15 of AAW14499 with a fragment corresponding to t
                                                                                                                                                                                                                                                                                                                              102. 206
/label= loop 3 modification region
                           fragment; claim 32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment; claim 23"
   a variant, c
or replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .313
                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the mature Aspergillus oryzae alpha-amylase (A). Variants of parent termamyl- and fungamyl-like alpha-amylases (and methods of constructing them) are claimed. Examples of variants are featured above. The variants have altered properties such as calcium dependency, substrate binding and stability. Also one or more proline or cysteine residues in the variant is modified or replaced with a non-proline or non-cystein residue such as alanine. The variants can be used for (dish) washing, as detergent additives or for fabric desizing or starch liquefaction. They can also be used for the production of search liquefaction. See also AAW14498-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                             methods of production - have altered dependency, substrate binding and stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 WITPUTAQIPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVVKNEMYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYONVMDGVLNYP1YYPLLLNAFKSTSGSMDDLYNM1NTVKSDCPDSTLLGTFVENHDNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2572; DB 2;
Pred. No. 1.9e-216;
                                                                                                                                                                   Borchert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 87-88; 171pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
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                                                                                                                                                                   Svendsen A, Bisgard-Frantzen
95DK-00000128.
95DK-00001192.
95DK-00001256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.8%;
                                                                                                                                                                                                                                                                             Alpha-amylase variants and properties such as calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.8
Matches 477; Conservative
                                                                                                            (NOVO ) NOVO-NORDISK AS
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                                                                                                                                                                                                                                                                                       The present invention describes polynucleotides which encode processing enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose isomerase, or glucoamylase) that are optimised for expression in plants. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic processing enzymes, which are activated under suitable conditions to act upon the desired substrate. Also described are self-processing transgenic plants and plant parts, e.g. grain, which express one or more of these enzymes and have an altered composition that facilitates plant and grain processing. Also described is a method (M) for converting starch to starch-derived products in a transformed plant part (TPP), by activating the starch processing enzyme contained in it. Transgenic grain is useful for preparing maltodextrin. A transformed plant (TPP) can be used to produce food produces having improved taste and to produce fermentable substrates for ethanol and fermented beverages. (M) eliminates the need to mill or physically disrupt the integrity of plant parts prior to recovery of starch-derived products. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140
                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding hyperthermophilic processing enzymes e.g. alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                          Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch; maltodextrin; ethano; fermentation; beverage; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                   Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
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                                                                                                                                                                                                                                                                                                               Kinkema
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                                                                                                                                                                                                                                                                                                               Craig
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Pred. No. 1.3e-215;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention
                                                                                                                                                                                                                                                                                                              Chen
                                                                                                                                                                                                                                                                                    (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 107; 158pp; English.
                                                                                                                                                                                                                                                                                                               Batie CJ,
                                                                                                                                                                                                                                  27-AUG-2002; 2002WO-US027129.
                                                                                                                                                                                                                                                            27-AUG-2001; 2001US-0315281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.7%;
                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.8
Matches 477; Conservative
                                                                                                                                        Aspergillus shirousami
                                                                                                                                                                                                                                                                                                               Basu SS,
                                                                                                                                                                                                                                                                                                                                       2003-268420/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1095 AA;
                                                                                                                                                                                                                                                                                                                                       WPI; 2003-268420/
N-PSDB; ACC44572.
                                                                                                                                                                              WO2003018766-A2
                        02-JUN-2003
                                                                                                                                                                                                                                                                                                               Lanahan MB,
                                                                                                                                                                                                       06-MAR-2003
                                                                                                                                                       Synthetic.
ABP96630
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                                                                                                                         300
                           240
                                                                            320
                                                                                                                                                                          FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
                                                                                                                                                                                                                       301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
                                                                                                                                                                                                                                                                       LIASANAIRNYAISKOTGFVTYKNWPIYKODTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
                                                                                                                                                                                                                                                                                                   LIASANAIRNYAISKDIGEVIYKNWPIYKDDITIAMRKGTDGSQIVTILSNKGASGDSYT 420
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                                                                                                                                                                                                                                                                                                                                                                     LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
                                                                                                                                                                                                                                                                                                                                                                                                 LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478
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PYQNVMDGVLAYPIYYPLLAAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant alpha-amylase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for detergents, dishwashing agents and liquefaction agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred, No. 1.1e-214;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 7; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92DK-00000946.
92DK-00001503.
93DK-00000292.
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Best Local Similarity 99.4
Matches 475; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-048855/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus oryzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1993;
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18-JUL-1994
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200 180 260 240

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This sequence represents the mature form of taka-amylase from A. oryzae. This sequence was used in a method for the generation of mutant pullulanases for use in the food industry (see also AAR79026-28). The wild type pullulanase enzyme was modified by the method of the invention for enhancing the hydrophobicity of a selected site of the pullulanse. The method comprises replacement of a group in the selected site with a hydrophobic group, replacement of an amino acid with a hydrophobic and/or insertion or deletion of a hydrophobic amino acid, and/or insertion or deletion of a hydrophobic amino acid from the selected site. The method was used to produce neopullulanases Y377F,
                                                                                                                                                                                                                                                                                                                                                                                                                                           PYONVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FASYTNDIALAKNVAAFIILNDGLPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
co-ordinate data; 3 dimensional structure.
                                                                                                                                                                                                                                                                                                  61 WITPVTAQLPQDCAYGDAYTGYWQTDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                                                                                                                                                                                    DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                       NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
                                                                                                                                                                                                                                                                                   81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                                                                                                                                                                                                                         DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
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                                                                                                                                                                           Score 2503.5; DB 2;
Pred. No. 2e-210;
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                                                                                                                                                                           eary Match 93.3%; set Local Similarity 97.9%; ttches 468; Conservative
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                                                                                                                                                                                             DVVKNEWYDWVGSLVSNYSIDGERIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                        WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                                                                PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
                                                                                       DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                   ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIDKLDYIQGMGFTAI
                                                                                                                          NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
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                                                                                                                                                                                                                                                                                                                                                                                                       LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS
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ABB80177 standard; protein; 495 AA.

ABB80177

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2.2.1.133) having improved transplaces manufacturing mattered in a crystallisation and the three dimensional structure of maltogenic amylase. Manufacturing maltogenic amylase comprises the following using crystallisation and the three dimensional structure of maltogenic amylase comprises the following steps:

(i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC 5027BP) and inserting the gene into plasmid pUCl9 to construct recombinant DNA (pThMA119); (ii) inserting the recombinant DNA to hours in Luxia-Bertani (IB) media and centrifuging the media to obtain a microbial cell; (iii) suspending the microbial cell with buffer solution at pH 7.5 and obtaining supernatant; and (iv) passing the supernatant through column chromatography and obtaining purified maltogenic amylase. The maltogenic amylase is a dimer comprised of two maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase (THMA) crystal. The amplase has a structure containing an activated region that consists of amino acid residues of Asp. 328, Glu-357, Asp-424, and a pocket with glucose bound that consists of amino acid residues of amino acid residues of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein (TAA), given in comparison with ThMA in the present invention
                                                                                                                                                                                                                                                                                                                                                                           Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes manufacturing maltogenic amylase
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(POST-) POSTECH FOUND.
(SAMY-) SAMYANG GENEX CORP.
                                                                                                                                                                                                                                                                    WPI; 2001-534477/59
                                                                                                                                                                  Park GH;
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                                                                         25 DWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWITP
                                                                                                                   85 VTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHMG
                                                                                                                                                                                                                                                                                                VMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASY
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Query Match

80.1%; Score 2151; DB 4; Length 423;
Best Local Similarity 95.7%; Pred. No. 1.4e-179;
Matches 405; Conservative 2; Mismatches 16; Indels
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The sequences given in ABB80164-87 show enzymatic proteins derived from A. fumigatus. These proteins display the catalytic activity of an enzyme such as transaes, callulase, glucose oxidase, glucoamylase, phytase, betagalactosidases, invertaes, lipase, alpha-amylase, laccase, betagalactosidases, invertaes. Lapase, alpha-amylase, laccase, betagalactosidases, invertaes. Compositions comprising the amount of compositions comprising cellulase are ester linkage in a composition. Compositions comprising cellulase are useful for modulating the amount of cellulose in a composition. Compositions comprising comprising composition composition. Compositions comprising composition. Compositions comprising comprising the amount of lactose in a composition. Compositions comprising beta-galactosidases are useful for modulating the amount of lactose in a composition. Compositions comprising the amount of sucrose in a composition. Compositions comprising lipase are useful for modulating the amount of sucrose in a composition composition compositions comprising comprising the amount of sucrose in a composition c
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                                                                                                                                                                                                                                            beta-galactosidase; invertase; lipase; alpha-āmylase; laccase; polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; maltodextrin, oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents.
                                                                                                                                                                                                                Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
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N-PSDB; ABQ80345, ABQ80346.
                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus fumigatus.
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16-AUG-2001; 2001EP-00000383.
16-AUG-2001; 2001EP-00000384.
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Matches 364; Conservative
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                                                                                                                                           WQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLK 121
                                                                                                                                                                             ALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQV 181
                                                                                                         61
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  having
                                                                                                                                                                                     patterns, and to raise anti-protein antibodies. The polypeptide having tannase activity increases the yield of tea liquor from tea leaves, improves the colour, flavour and health benefits of tea products, particularly an instent tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions
                                                                                                                                                                                                                                                  AAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLANAFKSTSGSMDDLYNMINTVKS
                                                                                                        2 VAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGT
                                                                                                                   EDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNK
                                                                                                                                                                                                                                                                                                                                DCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDP
                                                                                                                                                                                                                                                                                                                      ANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTD
                                                                                                                                                                                                                                                                                                                                                         GSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPR
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-amylase, enzyme, endohydrolysis, 1,4-alpha-glucosidic linkage; oligosaccharide; polysaccharide; baking.
                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of an alpha-amylase of Aspergillus niger.
                                                                      Length 495;
                                                                                      Indels
                                                                     78.2%; Score 2100; DB 6; 78.6%; Pred. No. 5.3e-175; iive 39; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 494
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16-AUG-2001; 2001EP-00000380.
16-AUG-2001; 2001EP-00000381.
                                                                                                                                                                                                                                                                                                                                                                                           VLYPTEKLAGSKICS 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2002; 2002WO-NL000522
                                                                   Query Match
Best Local Similarity 78.6'
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                      | ||| | || || || veyptaglingstvct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP97894 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus niger.
                                                     Sequence 495 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                            Aspergillus niger. Alpha-amylase enzyme of the filamentous functions and any any and any any any and alpha-amylase polynucleotides and polypeptides of the invention are useful in a baking process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STLLGTFVENHDNPRFAKSYTSDMSLAKNAATFTILADGIPIIYAGQEQHYSGGNDPYNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ALHSRGMYLMVDVVANHMGHNGTGSSVDYSVYRPFNSQKYFHNLCMISDYNNQTNVEDCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EATWISGYPIDSELYKLIASANAIRNYAISKDIGFVIYKNWPIYKDDTIIAMRKGTDGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 SLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLLGTFVENHDNPRFA-SYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANR
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                    fungus, preferably Aspergillus
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                                                                                                                                                                                                                                                                                                     Length 494;
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 Albermann
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                                                                                                                                                                                                                                                                                                 75.0%; Score 2012; DB 6; 73.8%; Pred. No. 2.8e-167; ive 62; Mismatches 65;
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:
Folkers
                                                                  New polynucleotide from a filamentous
niger, useful in a baking process.
                                                                                                                      Claim 13; Page 61-63; 81pp; English
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53 62

Gaps

9

Length 630; Indels 239 242 299 302

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Claim 17; Page 139-40; 169pp; English.
                       textile; tea liquor; cleaning ability
                                                                      Roemer T,
                                                 05-AUG-2002; 2002WO-US024842.
                                                        03-AUG-2001; 2001US-0309870P
                                                                                N-PSDB; ABQ80347, ABQ80348.
                                                               (ELIT-) ELITRA PHARM INC
                             Aspergillus fumigatus.
                                                                      Storms R,
                                                                            2003-332729/31
                                    WO2003012071-A2
                                           13-FEB-2003.
                                                                     Jiang B,
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KSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ethanol production; starch; fermentation; liquefaction; alpha-amylase;
fuel alcohol; fuel additive; neutral spirit; industrial ethanol; enzyme.
                                                                                                                                                                      3 WISQLFPLSLCSSLLGQAAHALTPAEWRSQSIYFLLTDRFGREDNSTTAACDVTQRLYCG
                                                                                                                                                                                                                                                                                                                                                                                              LKALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQT
                                                                                                                                                                                                                                                                                                                                                                                                                             180 QVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 NKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 NDAAGVYCVGEVFSGDPQYTCPYQNYLDGVLAYPIYYQLLYAFQSTSGSISNLYNMISSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 DPANREAVWLSGYSTSATLYSWIASTNKIRKLAISKDSAYITSKNNPFYYDSNTLAMRKG
                                                                                                                                    WSLFLYGLQVAAPAL----AATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCG
                                                                                                                                                                                                                                                                 GTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKG
      68.4%; Score 1835; DB 6;
66.8%; Pred. No. 1.4e-151;
iive 59; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus niger alpha-amylase protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE24207 standard; protein; 484 AA
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LPRVFVPSSWVSGSGLCGDS 502
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21-NOV-2000; 2000US-025213P.
11-DEC-2000; 2000DK-00001854.
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15-DEC-2000; 2000US-0256015P
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Query Match
Best Local Similarity 66.8
Matches 334; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus niger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unch as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
galactosidases, invertase, lipase, alpha-amylase, laccase,
polygalacturonase or xylanase. Compositions comprising the tannase are
useful for modulating the amount of compounds that comprise a gallate
ester linkage in a composition. Compositions comprising the
amount of glucose or oxyden in a composition.

Compositions comprising glucose oxidase are useful for modulating the
amount of glucose or oxyden in a composition. Compositions
phytase are useful for modulating the amount of myo-inositol phosphates
in a composition. Compositions comprising beta-galactosidases are useful
for modulating the amount of lactose in a composition. Compositions
comprising sucrase or invertase are useful for modulating the amount of
sucrose in a composition. Compositions comprising lipase are useful for
modulating the amount of glyceride in a composition. Compositions
comprising alpha-amylases are useful for modulating the amount of
starches or maltodextrins in a composition. Compositions
comprising alpha-amylases are useful for modulating the amount of
starches or maltodextrins in a composition. Composition
comprising alpha-amylases are useful for modulating the amount of
starches or maltodextrins in a composition. Compositions
comprising alpha-amylases are useful for modulating the amount of
starches or maltodextrins in a composition. Compositions
comprising alpha-amylases are useful for modulating the amount of
starches or maltodextrins in a composition. Compositions
comprising and composition composition compositions
comprising alpha-amylases are useful for modulating the amount of
starches or maltodextrins in a composition composition.
                       Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase; beta-galactosidase; invertase; lipase; alpha-amylase; laccase; polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; maltodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences given in ABB80164-87 show enzymatic proteins derived from funigatus. These proteins display the catalytic activity of an enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bussey H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 630 AA;
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The invention relates to a method for producing ethanol from starch-containing material, by fermentation. The method involves carrying out a secondary liquefaction step in the presence of a thermostable acid alphamylase. The method is used in producing ethanol from a starch-containing material such as tubers, roots or whole grain (e.g. corn, wheat or barley or their combination) or combination of the materials. Preferably ethanol is produced from starch-containing material that is obtained from cereals or from corns, cobs, wheat, barley, rye, milo and potatoes or their combination. The ethanol produced by above mentioned method is used as fuel alcohol and/or fuel additive. The ethanol is also useful as drinking ethanol i.e., potable neutral spirits or industrial ethanol. The present sequence is Aspergillus niger alpha-amylase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
                 Producing ethanol from starch-containing material e.g., tubers, roots, whole grain, for use in fuel, by fermentation comprises carrying out a secondary liquefaction step in the presence of a thermostable acid alpha-
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                                                                                                        Claim 35; Page 31-33; 33pp; English.
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Matches 318; Conservative
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Production of alcohol product, e.g. beer, comprises holding slurry of water and granular starch in presence of acid alpha-amylase and glucoamylase followed by simultaneous saccharification and fermentation.

9; SEQ ID NO 1; 43pp; English

Claim

Festersen RM;

Pedersen S,

Olsen HS,

WPI; 2004-677503/66.

(NOVO ) NOVOZYMES AS

10-MAR-2004; 2004WO-DK000154 10-MAR-2003; 2003US-0453326P

Aspergillus niger. WO2004080923-A2

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                                                                                                                                                                                                                                                                                                   product by holding a slurry of water and granular starch in the presence of an acid alpha-amylase and a glucoamylase at 0-20 deg C below the initial gelatinization temperature of the granular starch; holding the slurry in the presence of acid alpha-amylase, glucoamylase and yeast at 10-35 deg C to produce ethanol; and optionally recovering the ethanol. The method is used for the production of an alcohol product such as beer or recovered ethanol, e.g. fuel ethanol, potable ethanol or industrial ethanol. This sequence represents an acid fungal alpha-amylase from Aspergillus niger used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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443

384 SANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSL 

423

498

SGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 

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424

enzyme; alcohol; slurry; water; granular starch; acid alpha-amylase;
glucoamylase; gelatinization; yeast; beer; fuel ethanol; potable ethanol;
industrial ethanol.

Aspergillus niger acid alpha-amylase for ethanol production method

(first entry)

Ā

484

ADS75939 standard; protein;

Search completed: November 7, 2005, 18:57:39 Job time : 295.301 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 7, 2005, 18:40:32 ; Search time 57.6834 Seconds (without alignments) 830.671 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-820-200-2
2684
1 MVAWWSLFLYGLQVAAPALA......LPRVLYPTEKLAGSKICSSS 498

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

.283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Descrip	alpha-amylase (EC	alpha-amylase (EC	_	атујаве (	атујаве (			alpha-amylase (EC	ø	pullulanase (EC 3.						alpha-amylase a pr	١	probable alpha-amy	a-a	alpha-amylase - fi		o)	beta-amylase (EC 3	alpha-amylase homo	cyclomaltodextrin	cyclomaltodextrin	cyclomaltodextrin	ü	alpha-amylase (EC
ID	ALAS1	JS0663	ALAS3	B48305	JN0588	A48305	JT0466	JK0201	A35282	JC4510	833921	806115	S23355	ALBYAF	S72270	T38770	T41603	T38448	S62505	T41503	T40860	S31478	A29130	T39539	AI1827	ALBSG1	ALBSG3	ALBSG7	ALBSK
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Length	499	499	499	499	499	498	499	478	484	624	507	512	512	494	631	513	625	491	581	564	478	482	1196	774	642	713	712	713	528
% Query Match	100.0	99.7	99.6	99.6	99.6	99.5	99.0	93.3	66.3	60.7	56.9	54.0	53.9	52.1	47.1	37.8	35.9	34.3	33.5	33.5	33.5	•		24.3	17.9	17.0	16.9	•	16.4
Score	2684	2675	2674	2674	2673	2662	2656	2503.5	1780	1629	1527	1449	1445.5	1397.5	1264	ŧΩ	963.5	920.5	899		868	m	670	m	Ч	56	454.5	4	440.5
ω <u>.</u>	-	7	m	4	2	9	7	80	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

cvclomaltodextrin	cyclomaltodextrin	cyclomaltodextrin	alpha-amylase (EC	cyclomaltodextrin	cyclomaltodextrin	cyclomaltodextrin	alpha-amylase (EC	glycosyl hydrolase	cyclomaltodextrin	cyclomaltodextrin	cyclomaltodextrin	cyclomaltodextrin	cyclomaltodextrin	cyclomaltodextrin	alpha-amylase (EC
863598	ALKBG	ALBSX1	S28179	A58800	ALBSGR	809196	S28784	G75392	I39805	ALBSGC	ALBSG6	ALBSXR	ALBSMX	ALBSXF	A60999
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710	655	703	919	713	714	713	717	483	704	718	718	713	718	711	1104
16.1	16.0	15.9	15.8	15.6	15.6	15.4	15.4	15.3	15.2	15.1	15.1	15.1	14.9	14.3	14.0
433	428.5	428	424.5	418	418	414.5	412	410	407	406.5	405.5	405	399.5	384.5	376.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 ALASI alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
N'Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A C:Species: Aspercillus orvzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004 C;Accession: S04548; A33214; \(\overline{3}\)S0240; A91930; A93767; A10\(\overline{6}\)Z7
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon on A;Reference number: S04548; MUID:89237897; PMID:2785629
A; Molecule type: DNA
A;Residues: 1-499 <wir></wir>
A)CLOBB-IELDIEGES: UNIFROI:FIUSZO; EMBD:AIZ/35; NID:96450; FIUM:CM31210:1; FIU:9430450; A;Genetics: AMYI
A;Acceвsion: A33214 A;Molecule type: mRNA
A;Residues: 1-499 <wi2></wi2>
A;Cross-references: GB:X12725; NID:g2430; PIDN:CAA31218.1; PID:g293921 R:Genes. M.J.; Dove, M.J.; Seliqv, V.L.
Gene 79, 107-117, 1989
A; Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing
Afreteration: USO240; MULD:093/0/0/; FMLD:2/09102 Afreteration: USO240
A; Molecule type: DNA
A;Residues: 1-499 cGEN>
A.Note: the authors refer to this as isozyme II
R;Isemura, S; Ikenaka, T.
J. BLOCHEM. '4', I-1', I
A;Accession: A91930
A; Molecule type: protein
A;Keslūtes: VD-ZZS <ise> R;Narita, K.</ise>
Proc. Jpn. Acad. 51, 285-290, 1975
A;Keterence number: A93/6/ A;Accession: A93/67
A; Molecule type: protein
A;keBidueB: 434-443,446-447,'Q',449-456,'GIN',459-464,'40/-460,' B',470, B',472-459 KNAN R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A. A:Reference number: A17454: MIID:84212370: PMID:6609921
R;Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkenburg, J.P.; Wilkinson, A submitted to the Brookhaven Protein Data Bank, August 1992
A;Reference number: A51548; PDB:6TAA
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-49/ C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics: <amy1></amy1>

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A;Gene: amy1
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Genetics: -AMY2>
A;Gene amy2; Amy1
C;Genetics: -AMY2>
A;Gene: amy2; Amy1
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/stach degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polys
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; F;1-21/Domain: signal sequence #status predicted <SIC>
F;22-499/Product: alpha-amylase 1 #status experimental <AMT>
F;194-31/Domain: alpha-amylase core homology <AMY>
F;194-31/Domain: alpha-amylase core homology <AMY>
F;15-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Aan, Gu, Aap, His) #status predicted
F;227,251,318/Active site: Asp, Glu, Asp #status predicted
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JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C.Species: Aspergillus sp.
C.Species: Aspergillus sp.
C.Species: Angelgog #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C.Accession: JS0663
R.Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Bloctchnol. Blochem. 56, 174-179, 1992
A.Fitle: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase CDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase CDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase CDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase CDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase CDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase CDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase CDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase CDNA of Aspergillus shirousamii and its expression A.Fitle: Cloning of the alpha-amylase CDNA of Aspergillus shirousamii and its expression control of the alpha-amylase CDNA of Aspergillus shirousamii and its expression control of the alpha-amylase CDNA of Aspergillus shirousamii and its expression control of the alpha-amylase CDNA of Aspergillus shirousamii and its expression control of the alpha-amylase CDNA of Aspergillus shirousamii and its expression control of the alpha-amylase CDNA of Aspergillus shirousamii and its expression control of the alpha-amylase CDNA of Aspergillus shirousamii and its expression control of the alpha-amylase CDNA of Aspergillus shirousamii and its expression control of the alpha-amylase CDNA of Aspergillus shirousamii and its expression control of the alpha
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100.0%; Pred. No. 7e-185;
ive 0; Mismatches 0
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Matches 498; Conservative
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Alternate manes (BC 3.2.1.1) 3 precursor - Aspergillus oryzae

N.Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A

S.Abternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A

C; Becession: So6549; A33215; A44713

R; Wirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.

Mol. Microbiol. 3, 3-14, 1989

A; Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon o A; A; Reference number: S04549; MUID:89237897; PMID:2785629

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-499 < WIR>
A; Accession: A33215

A; Accession: A32215

A; Accession: Accessio
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Kgenes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/etarch degradation C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology C;Keywords: glycoprotein; glycoaidase; hydrolase; polysaccharide degradation F;1-21/Domain: signal sequence #status predicted <SIG>F;2-49/Product: alpha-amylase #status predicted <ALP>F;194-321/Domain: alpha-amylase core homology <AMY>F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
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alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
NyAlternate names: Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JN0588
R;Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kirita, N.; Tsuboi, A.; Udaka, S.
Gene 84, 319-327, 1989
A;Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for m
A;Reference number: JN0588; MUID:90128276; PMID:2612911
                                                                                 two alpha-amylase genes from Aspe
                                      K.H.; Royer,
                                                                                                                                                                                                                       A.Cross-references: UNIPROT:Q02906
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology
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       C;Accession: B48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Koc Curr.; Genet. 17, 203-212, 1990
A;Title: Gloning, characterization, and expression of two alpha-A;Reference number: A48305; MUID:90254827; PMID:3340591
A;Accession: B48305
A;Status: preliminary; not compared with conceptual translation A;Rolecule type: DMA
A;Residues: 1-499 < KOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 3.7e-184;
0; Mismatches 2;
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A,Residues: 1-499 <TSU>
A,Cross-references: UNIPROT:Q96TH4
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Best Local Similarity 99.6%;
Matches 496; Conservative (
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A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: A4713
A;Roclecule type: DNA
A;Residues: 1-499 cGEN>
A;Note: the authors refer to this as isozyme I
A;Note: the authors refer to this as isozyme I
B; Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytric residues of Taka-amylase A.
A;Title: Structure and possible catalytric residues of Taka-amylase A.
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
C;Comment: one atom of calcium per molecule is essential for activity.
C;Genetics:
A;Gene: amy3; AmyI
A;Introns: $6/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C;Superfamily: Aspergallus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; predicted csIG-Fi22-499/Product: alpha-amylase core homology csAMy>
F;121/Domain: alpha-amylase core homology candy:
F;121/Domain: alpha-amylase core homology candy:
F;149.183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F;142.183,196,231/Binding site: carbohydrate (Asn, Glu, Asp, His) #status predicted
F;218/Binding site: carbohydrate (Asn, Glu, Asp, His) #status seperimental
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C;Species: Aspergillus awamori
C;Date: 03-Peb-1994 #sequence_revision 03-Peb-1994 #text_change 09-Jul-2004
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A48305
alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asper A;Reference number: A48305
A;Accession: A48305
A;Accession: A48305
A;Accession: A48305
A;Accession: A48305
A;Residues: I-498 cKOR>
A;Residues: I-498 cKOR>
A;Cross-references: UNIPROT:Q02905
C;Function:
A;Poscription: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C; Comment: The alpha amylases are encoded by multigene lamily.
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; The Taa-Gi
A; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
A; Description:
C; Function:
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Description:
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Reywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F; 1-21/Domain: signal sequence #status predicted <SiG>F; 22-499/Product: alpha-amylase #status predicted <MAT>F; 194-321/Domain: alpha-amylase core homology <AMY>F; 198-321/Domain: alpha-amylase core homology <AMY>F; 218/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 4.3e-184;
0; Mismatches 2; Indels
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Best Local Similarity 99.6%;
Matches 496; Conservative
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NiAlternate names: glycogenase; Taka-amylase A
C;Specia: Aspergillus oryzae
C;Specia: Aspergillus oryzae
C;Specia: Aspergillus oryzae
C;Bate: 3. Haar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JT0466
R;Tada, S; Jimura, Y; Gomi, K; Takahashi, K; Hara, S; Yoshizawa, K.
Agric, Biol. Chem. 53, 593-599, 1989
A;Ttle: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergia A;Recession: JT0466
A;Accession: JT0466
A;Acc
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C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>
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                                                                                                                                                                      99.2%; Score 2662; DB 2;
99.6%; Pred. No. 2.7e-183;
iive 0; Mismatches 2;
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Best Local Similarity 67.2
Matches 319; Conservative
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C; Species: Aspergillus oryzae
C; Species: Jr0201
R; Toda, H: Kondo, K: Narita, K.
R; Toda, H: Kondo, K: Narita, K.
R; Toda, H: Kondo, K: Narita, K.
R; Feference number: Jr0201
A; Reference number: Jr0201
A; Reference number: Jr0201
A; Reference number: Jr0201
A; Residues: 1-478 «TOD>
A; Cross-references: UNIPROT: P10529
C; Comment: One atom of calcium per molecule is essential for the activity.
C; Comment: One atom of calcium per molecule is essential for the activity.
C; Comment: This enzyme is a glycoprotein.
C; Comment: See also PIR: Jr0466 and PIR: JS0240.
C; Comment: See also PIR: Jr0466 and PIR: JS0240.
C; Comment: See also PIR: Jr0466 and PIR: JS0240.
C; Comment: See also PIR: Jr0466 and PIR: JS0240.
C; Superfamily: Aspergillus alpha-amylase: alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase core homology c, Reyvords: glycoprotein; glycosidaes; hydrolase; polysaccharide degradation
C; Superfamily: Aspergillus alpha-amylase core homology c, Reyvords: glycoprotein; glycosidaes; hydrolase; polysaccharide degradation
F; 173: 300/Domain: alpha-amylase core homology c, Reyvords: glycoprotein; glycoprotein; glycosidaes; hydrolase; 
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                                     Query Match 99.0%; Score 2656; DB 2; Length 499; Best Local Similarity 99.4%; Pred. No. 7.2e-183; Matches 495; Conservative 0; Mismatches 3; Indels
F;231,251,318/Active site: His, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-amylase (BC 3.2.1.1) - Aspergillus oryzae
N.Alternate names: Qlycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498
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Best Local Simi
Matches 468;
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Apparation: Aspergillus niger
C;Species: Asservation: Asservation 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: Asservation: Asservation 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: Asservation: Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pet
Biochemistry 29, 6244-6249, 1990
A;Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom
A;Reference number: A35282
A;Stecence number: A35282
A;Stecence number: A35282
A;Stecence number: Asservation acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residuae: 1-484 <BOBS
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pethway: glycogen/fetarch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolyse; polysaccharide degradation
F;173-300/Domain: alpha-amylase core homology <AMY>
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1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQXYCGGTWQGIIDKLDYLQGMGFTAI
                                                                                                                                                                                                  NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
                                                                                                                                                                                                                                                                                                                        DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                                                                                                                                                                                                                                              DVVKNEMYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS
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67.2%; Pred. No. 5.1e-120;
cive 63; Mismatches 93;
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501

561

441

494

621

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C;Species: Schwanniowyces occidentalis
C;Date: 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S33921
R;Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
Curr. Genet. 24, 75-83, 1993
A,Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase fro A;Reference number: S33921; MUID:93365041; PMID:8358835
A;Accession: S33921
A;Molecule type: DNA
A;Molecule type: DNA
A;Residences: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g3965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Gene: SWA2
C.Function:
A.Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A.Pathway: glycogen/starch degradation
A.Pathway: glycogen/starch degradation
C.Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C.Superfamily: Aspergillus alpha-amylase; hydrolase; polysaccharide degradation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-50/Product: alpha-amylase = #status predicted <MAT>
F;20-50/Product: alpha-amylase core homology <AMY>
F;20-50/Product: alpha-amylase core homology <AMY>
F;21-50/Pomain: alpha-amylase (AMY>
F;21-50/Pomain: alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternate names: alpha-1,4 glucanohydrolase schwanniomyces occidentalis) species: Schwanniomyces
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             DVNTQLDTVKSEYQSWVKQLIANYSIDGLRIDTVKHVQMDFWAPFQEAAGIYTVGEVFDG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
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                                                                                                                   ||:|||||| :||||||||:|||:|||:||| DPSYTCPYQENLDGVLNYPVYYPVVSAFQRVGGSISSLVDMIDTLKSECIDTTLLGSFLE
                                                                          DPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVE
                                                                                                                                                                                                                                            NODNPRFPSYTSDESLIKNAIAFTILSDGIPIIYYGQEQGLNGGNDPYNREALWPTGYST
                                                                                                                                                                                                                                                                                                                                    DSELYKLIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGA
                                                                                                                                                                                                                                                                                                                                                                      502 TSTFYEYIASLNQIRNHAIYIDDTYLTYQNWVIYSDSTTIAMRKGFTGNQIITVLSNLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 SGSSYTLTLSNTGXTASSVVXELLTCTAVTVDLSGNLAVPMSGGLPRVFYPESQLVGSGI
                                                                                                                                                                                                       315 NHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPT
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57.7%; Pred. No. 7.8e-102;
iive 74; Mismatches 130;
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CG4510

Nyllternate names (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)

Nyllternate names (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)

Nylternate names i.Mx1 protein; raw starch-degrading amylase

Nylociasins alpha-daxtrin endo-1.6-alpha-glucosidase (EC 3.2.1.41)

C;Species: Lipomyces kononenkoae endo-1.6-alpha-glucosidase (EC 3.2.1.41)

C;Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004

C;Accession: U.C.; Marnur, J.; Pretorius, I.S.

A;Reference number: JG4510; WUID:96105202; PMID:8529895

A;Title: Cloning, sequence analysis and expression in yeasts of a CDNA containing a Lipomyces for a Company of the Company o
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RTIWYDWVADLVSNYSVDGLRIDSVLEVEPDFFPGYQEAAGVYCVGEVDNGNPALDCPYQ
                                                                                                  244 KVLDGVLAYPTYWQLLYAFESSGGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPRFAS
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C;Species: Saccharomycopsis fibuligera
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
R;ItOh, T.; Yamashita, I.; Fukui, S.
FEBS Lett. 219, 339-342, 1987
A;Title: Nucleotide sequence of the alpha-amylase gene (ALP1) in the yeast Saccharomyco:
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A,Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-512 < wurs>
A;Cross-references: UNIPROT:P19269; EMBL:X62079; NID:g4880; PIDN:CAA43995.1; PID:g4881
A;Cross-references: UNIPROT:P19269; EMBL:X62079; NID:g4880; PIDN:CAA43995.1; PID:g4881
A;Cross-references: UNIPROT:P19269; EMBL:X62079; NID:g4880; PIDN:CAA43995.1; PID:g4881
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase; core homology
C;Keywords: glycoprotein; glycosidase; hydrolase
F;209-336/Domain: alpha-amylase core homology <AMY>
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  396 ELISKLNQIRNQAIKKDSAYSTYKSSVVSSSDHYIATRKGSDANQLISIFNNLGSNG-SQ 454
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                                                                                                                                                                                                                                                    alpha-amylase (EC 3.2.1.1) precursor - yeast (Schwanniomyces occidentalis) C;Species: Schwanniomyces occidentalis C;Species: Schwanniomyces occidentalis C;Accession: S23855 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S23855 R;Wu, F.M.; Wang, T.T.; Hau, W.H. FEMS Microbiol. Lett. 82, 313-318, 1991 A;Ttle: The nucleotide sequence of Schwanniomyces occidentalis alpha-amylass A;Reference number: S23355
                                                                                                                 511
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                                                           TLSLSGAGYTAGOOLTEVIGCTTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS
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C; Species: Schwanniomyces occidentalis
C; Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C; Accession: S06115
R; Strasser, A.W.M.; Selk, R.; Dohmen, R.J.; Niermann, T.; Bielefeld, M.; Seeboth, P.; Tu Eur. J. Biochem. 184, 699-706, 1989
A; Title: Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the secre A; Recession: S06115
A; Recession: S06115
A; Rocession: S0615
A; Rocession: S06115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 YNHYAWNGDGSSVDYSSFTPFNQQSYFHDYCLIINYNDQTNVEDCWEGDTEVSLPDLSTE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 IWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 ANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 KDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-amylase (EC 3.2.1.1) AMY1 precursor - yeast (Schwanniomyces occidenta C;Species: Schwanniomyces occidentalis C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004 C;Accession: S06115
                                                        SDCKDITLLGNFIENHDQPRLPSYTSDSALIKWAIAFNLMSDGIPIIYYGQEQGYSGSSD
                                                                                                                                                                      DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP
                                                                                                                                                                                                                                                                                       | :||:::|| | | | | | ::| | DDQRIVSVFNNLGSSG-SQTVTFS-TKYSGGEKVVDVLTCQTSYANSDSTLTVSISGGAP
                                                                                                                                        PANREATWLSGYPIDSELYKLIASANAIRNYAISKDTGFVTYKWWPIYKDDTTIAMRKGT
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Best Local Similarity 56.4%; Pred. No. 3.1e-96;
Matches 269; Conservative 74; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                     496
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A;Accession: S72270
A;Molecule type: DNA
A;Residues: 1-631 <IEF>
A;Cross-references: UNIPROT:Q92394; EMBL:D83540; NID:g1595852; PIDN:BAA12010.1; PID:g155
A;Experimental source: strain S-2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: November
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                                                 A/Rocession: S00064

A/Roces references: UNIPROT: P21567; EMBL: X05791; NID: 94847; PIDN: CAA29233.1; PID: 94848

A/Roces: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Thr

C/Genetics:
A/Gene: ALP1

C/Function:
A/Ponetics:
A/Ponetics: A/Roces fracth degradation

C/Superfamily: Appergillus alpha-amylase; alpha-amylase core homology

C/Reywords: calcium; extracellular protein; glycoprotein; glycosidase; hydrolase; metall

F/27-494/Product: alpha-amylase #status predicted AMA7

F/200-227/Domain: alpha-amylase from homology AMA7

F/200-227/Domain: alpha-amylase core homology AMA7

F/201-494/Product: alpha-amylase core homology AMA7

F/21-494/Product: alpha-amylase (ore homology AMA7)

F/21-494/Product: alpha-amylase (ore homology AMA7)
                                                                                                                                                                                                    Note: use sequence the management of internal 1,4-alpha-D-glucosidic bonds (Genetics). Function: start of gradation of internal 1,4-alpha-D-glucosidic bonds (Septembrity) apperallula alpha-amylase; alpha-amylase core homology (Superfamily) apperallular protein; glycoprotein; glycop
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37270
alpha-amylase (EC 3.2.1.1) precursor - Cryptococcus sp. (strain CS2)
C;Species: Cryptococcus sp.
C;Species: Cryptococcus sp.
A;Variety: strain CS2
A;Variety: strain CS2
A;Variety: strain CS2
C;Accession: S72270
B;Icfuji, H.; Chino, M.; Kato, M.; Iimura, Y.
Biochem. J. 318, 989-996, 1996
A;Title: Raw-starch-digesting and thermostable alpha-amylase from the yeast Cryptococcus A;Reference number: S72270; MUID:96433120; PMID:8836148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.1%; Score 1397.5; DB 1; Length 52.5%; Pred. No. 1.5e-92; ive 83; Mismatches 129; Indels
                             number: S00064; MUID:87276512; PMID:3497057
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Best Local Similarity
Matches 264; Conserv
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A.Gene: amy-CS2
A.Introns: 289/2; 326/2
A.Introns: 289/2; 326/2
C.Punction: 289/2; 326/2
A.Punction: 289/2; 326/2
A.Punction: 289/2; 326/2
C.Punction: 3.Puncopen/starch degradation
C.Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C.Superfamily: Aspergillus alpha-amylase; hydrolase; polysaccharide degradation
F.1.-20/Domain: signal sequence #status predicted <SIG>
F.21-631/Product: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                        KDFWPGYNKAA-GVYCIGEVLDGDPAYTCPYQNV-MDGVLNYPIYYPLLNAFKSTSGSMD
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49.2%; Pred. No. 8e-83;
iive 84; Mismatches IE
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251; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                      OM protein - protein search, using sw model
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Run on:

November 7, 2005, 18:24:00; Search time 267.266 Seconds (without alignments) 954.162 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-820-200-2
2684
1 MVAWWSLFLYGLQVAAPALA......LPRVLYPTEKLAGSKICSSS 498

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4		d			SUMMARIES	
Result	Score	Query Match	Length	DB	ID	Description
- - -	2684	100.0	498	2	076CT3	076ct3 asperdillus
7	2684	100.0	499	٦	AMYA ASPOR	9
e	2680	6.66	499	N	076L <u>9</u> 9	
4	2675	99.7	499	٦	AMY ASPSH	
ιΩ	2674	99.6	499	П	AMYB ASPAW	
9	2674	9.66	499	~	Q96TH4	4
7	2674	99.6	499	N	Q7LV45	
æ	2662	99.2	498	Н	AMYA ASPAW	
6	1826	68.0	490	~	Q9UV <u>0</u> 7	
10	1810	67.4	640	N	013296	
11	1791	66.7	634	N	Q76L96	Q76196 aspergillus
12	1778	66.2	484	٦	AMYA ASPNG	P56271 aspergillus
13	1725.5	64.3	623	~	6 <u>0</u> 0060	σ
14	1662	61.9	647	~	Q6YF33	
15	1629	0	624	Н	AMY1_LIPKO	
16	1527	56.9	507	Ч	AMY2_DEBOC	
17	1449	54.0	512	-	AMY1_DEBOC	
18	1397.5	52.1	494	~	AMY1_SACFI	P21567 saccharomyc
19	1272.5	47.4	492	~	Q7SD <u>J</u> 6	Q7sdj6 neurospora
20	1264	47.1	631	7	Q92394	Q92394 cryptococcu
21	1056.5	39.4	533	0		
22	1015.5	37.8	513	-	AMY3_SCHPO	
23	63	S	625	7	074922	
24	920.5	34.3	491	7	013996	
25	899	33.5	581	-	AMY1_SCHPO	
26	898.5	•	564	7	AMY 4_SCHPO	•
27	868	33.5	478	٦	YQ29_SCHPO	
28	895	33.3	499	~	Q8J1E4	Q8jle4 lipomyces k
29	737	27.5	482	~		
30	~	25.0	1196	٦	AMYB_PAEPO	<u>ო</u>
31	653.5	24.3	774	-	AMY2_SCHPO	042918 schizosacch

CSO CST CST CI ETU	2 Q8Z0C9 2 Q8ZMG0 2 Q8ZMG0 0 087FT5 1 CDGT_BACS3 1 CDGT_BACS3 2 Q9XZ11 2 Q6S3E3 2 Q9F5W3 2 Q9F5W3 2 CDGT_BAC11 1 AMY_BACS1 2 CDGT_BAC11 2 CDGT_THETU	00011001011000	17.9 642 2 0820C9 17.9 642 2 08R0C0 17.9 877 2 08RVG0 17.0 713 1 CDGT_BACS0 16.9 17.9 2 09XZ11 16.8 719 1 ANYM_BACST 16.7 712 2 06S3E3 16.7 713 2 09FSB3 16.7 713 2 09FSB3 16.6 713 1 CDGT_BACII 16.4 528 1 ANY_BACCI 16.1 10 1 CDGT_THETU	642 2 642 2 642 2 713 1 7198 2 712 713 2 713 1 7		P05618 bacillus sp	P09121 bacillus sp	Q9kz11 streptomyce	P19531 bacillue st	Q683e3 bacillus sp	Q9f5w3 bacillus ci	P30921 bacillus sp	PO8137 bacillus ci	Q82as4 streptomyce		Q8r900 thermoanaer
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 206-225.
MEDLINE=74001521; PubMed=4733850;
Isemura S., Ikenaka T.,
Isemura S., Ikenaka T.,
"The amino acid sequences of glycopeptides obtained from Taka-amylase
A with trypsin and chymotrypsin.";
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MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
Genes M.J., Dove M.J., Seligy V.L.;
"Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing eight introns.";
Gene 79:107-117(1989).
                                                                 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
                                                                                                                                                                                                                                                                                                                                                                                                   P10529; P11763; Q00250; 01-0CT-1989 (Rel. 12, Created) 01-0CT-1989 (Rel. 12, Last sequence update) 01-0CT-2004 (Rel. 45, Last annotation update) 25-0CT-2004 (Rel. 45, Last annotation update) alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-alpha-D-glucan glucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Takahashi K., Hara S., Yoshizawa K.; Tada S., Imura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.; "Cloning and nucleotide sequence of the genomic Taka-amylase A gene Aspergillus oryzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus oryzae.
Pukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-DSM 63303;
MEDLINE-89237897; PubMed-2785629;
Wirsel S., Lachmund A., Wildhardt G., Ruttkowski E.;
"Three alpha-amylase genes of Aspergillus oryzae exhibit identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toda H., Kondo K., Narita K.;
"The complete amino acid sequence of Taka-amylase A.";
Proc. Jpn. Acad., B. Phys. Biol. Sci. 58:208-212(1982)
                                                                                                                                                                                                                                                                                                                                                                                    499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agric. Biol. Chem. 53:593-599(1989)
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SEQUENCE OF 22-499.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at high concentrations.

SUBUNIT: Monomer.

SUBUNIT: Monomer.

SUBUNIT: Monomer.

SUBUNIT: Monomer.

Fermentability of beer worts (including those made from unmalted cereals), in the starch industry to make high maltose and high DE syrups (starch saccharification), in the alcohol industry to reduce fermentation time, in the cereal food industry for reduce fermentation and improvement of chilled and frozen dough, and in the forestry industry for low-temperature modification of starch. Sold under the name Fungamyl by Novozymes.

MISCELLANBOUS: The sequence of AMYl and AMY2 is shown.

SINILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-80227691; PubMed-6156152;
Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
Toda H., Narita K., Kakudo M.;
"Molecular structure of taka-amylase A. I. Backbone chain folding at
3-A resolution.";
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Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
Multigene family; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-84212370; PubMed-6609921;
Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
"Structure and possible catalytic residues of Taka-amylase A.";
J. Blochem. 95:697-702(1984).
                                                                                                                                Phys. Biol. Sci. 51:285-290(1975)
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                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
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EMBL; X12726; CAA31229.1; --
EMBL; X12727; CAA31220.1; --
EMBL; D00434; BAA00336.1; --
EMBL; M33218; AAA32708.1; --
PIR; JK0201; JK0201.
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6TAA; X-ray; @=22-499.
7TAA; X-ray; @=22-499.
Biochem. 74:1-10(1973).
                                                                                                                                Proc. Jpn. Acad., B,
                                                                SEQUENCE OF 433-499
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                                                                                              Narita K.;
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/FIId=CAR_000125.

0 -> R (in AMY3).
F -> L (in AMY3).
TT -> DC (in Ref. 5).
0 -> T (in Ref. 5).
0 -> Y (in Ref. 3).
P -> L (in Ref. 3).
0 -> Y (in Ref. 3).
0 -> Y (in Ref. 3).
1 -> L (in Ref. 3).
1 -> L (in Ref. 4).
1 -> L (in Ref. 4).
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  Length 499;
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Last annotation update)
    DB 1;
Query Match 100.0%; Score 2684; DB 1;
Best Local Similarity 100.0%; Pred. No. 2e-178;
Matches 498; Conservative 0; Mismatches 0;
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Q76199;
65-UU-2004 (TERMELRE1. 27, La
05-UUL-2004 (TERMELRE1. 27, La
05-UUL-2004 (TERMELRE1. 27, La
Alpha-amylase precursor.
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Aspergillus awamori. Bukaryota, Pungi; Ascomycota; Pezizomycotina; Burotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. NCBL\_TaxID=105351;

P SEQUENCE FROM N.A.

STRAIN=KT-11;

Matsubara T.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

L SUMILARITY: Belongs to family 13 of glycosyl hydrolases.

C -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

EMBL, AB083159; BAD6002.1; -
R GO; GO:0005955; P:alpha-amylase activity; IEA.

R GO; GO:0005955; P:carbohydrate metabolism; IEA.

R InterPro; IPR0066047; Alpha amyl cat.

R InterPro; IPR0066045; Alpha myl cat.

R InterPro; IPR0066046; Glyco hydro\_13.

R Pfan; PF00128; Alpha-amylase; 1.

R PRINTS; PR00110; ALPHAMYLASE.

R SWART; SM00642; Aamy; 1.

Potential. 2B357AE38B36C1C2 CRC64; 21 Pc 54794 MW;

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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                               Score 2675; DB 1;
Pred. No. 8.6e-178;
0; Mismatches 1;
   entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                 Interpro; IPR006589; Alp amyl_cat_sub.
Interpro; IPR006047; Alpha_amyl_cat.
Interpro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
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                              EMBL; D10461; BAA01255.1; -. HSSP; P10529; 7TAA.
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                      Gaps
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5070;
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   Length 499
                    Indels
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01-APR-1993 (Rel. 25, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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 Score 2680; DB 2;
Pred. No. 3.9e-178;
1; Mismatches 0;
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Query Match
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Matches 497; Conservative
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Calcium 1 (by similarity).

Calcium 1 (via carbonyl oxygen) (By similarity).

Calcium 1 (by similarity).

Calcium 2 (By similarity).

Calcium 1 (via carbonyl oxygen) (By similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

By similarity.

By similarity. 182 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL PANREATWLSGYPTDSELYKLIASANAIRNYAISKOTGFVTYKAWPIYKODTTIAMRKGT DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT Gaps SMART; SM00642; Aamy; 1. Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase; Hydrolase; Signal. . 0 Alpha-amylase. Nucleophile (By similarity). Proton donor (By similarity) 1; Indels Length

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DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP 480
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                   2 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
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Iimura Y.;
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Biosci. Biotechnol. Biochem. 64:816-827(2000).
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; ABO21876; BAA95703.1; -.
PIR; JN0588; JN0588.
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GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005798; F:hydrolase activity, acting on gl
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp amyl_cat.
InterPro; IPR006646; Glyco_hydro_l3.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
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MEDLINE=90254627; PubMed=2340591;

MEDLINE=90254627; PubMed=2340591;

MEDLINE=90254627; PubMed=2340591;

MEDLINE=90254627; Mard M., Wilson L.J., Berka R.H.,

ROYER T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.H.,

"Cloning, characterization, and expression of two alpha-amylase genes
from Aspergillus niger var. awamori.";

Curr. Genet. 17:203-212(1990).

-! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linkages in oligosaccharides and polysaccharides.
--- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
--- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolism; Glycoprotein; Glycosidase;
                                                                                                                                                                                                                         Aspergillus awamori.
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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Calcium 1 (By similarity).

Calcium 1 (via carbonyl oxygen) (By similarity).

Calcium 1 (By similarity).

Calcium 2 (By similarity).

By similarity.

By similarity.
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Pred. No. 1e-177;
0; Mismatches 2; Indels
                                                                                              01-0cT-1996 (Rel. 34, Created)
1-0cT-1996 (Rel. 34, Last sequence update)
25-0cT-2004 (Rel. 45, Last annotation update)
Alpha-amylase B precursor (RC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-amylase B.
Nucleophile (By similarity).
Proton donor (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM0642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism
Hydrolase; Multigene family; Botonis.
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59 By
185 By
304 By
496 By
218 N-
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Best Local Similarity 99.6%;
Matches 496; Conservative
                                                         STANDARD;
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                                                                                                                                                                                  glucanohydrolase B).
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231
                                                         AMYB ASPAW
                                                                                                                                                                                                            Name=AMYB;
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SEQUENCE
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             RESULT 5
AMYB_ASPAW
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Pfam, PF00128; Alpha-amylase; 1. PRINTS; PR00110; ALPHAAMYLASE. SMART; SM00642; Aamy; 1. Glycosidase; Hydrolase.
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(Rel. 34, Last seq
                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.6'
Matches 496; Conservative
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Name=AMYA;
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Fakhoury A.M., Woloshuk G.P.;

Fakhoury A.M., Woloshuk G.P.;

Fakhoury A.M., Woloshuk G.P.;

Fakhoury B.M., Woloshuk G.P.;

Fakhoury B.P.;

Fakhoury A.M., Woloshuk G.P.;

Fakhoury B.P.;

Fakhoury B.P.;

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Fakhoury B.P.;

Fakhoury A.M.;

Fakhoury B.P.;

Fakhoury B.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                        ö
                                                                                                                                                      DB 2; Length 499;
                                                                                                                                                                                                                        Indels
SMART; SM00642; Aamy; 1.
Glycosidase; Hydrolase.
SEQUENCE 499 Aa; 54804 MW; EEF42ADA71D20DA9 CRC64;
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Last annotation update)
                                                                                                                                                  Query Match 99.6%; Score 2674; DB 2; 1
Best Local Similarity 99.6%; Pred. No. 1e-177;
Matches 496; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z
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                                                                                                                                                                                                                                                                                                                                                                                       TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPPSSQDYFHPPCLIQNYEDQTQ
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-I. CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

-I. COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
                                                                                                                                                                                                                                                       MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADRKYCGG
                                                                                                                                                                                                            MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
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                                                                                                                                          Gaps
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                      Indels
                                                                     Length
499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;
                                                          99.6%; Score 2674; DB 2;
99.6%; Pred. No. 1e-177;
iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498 AA
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422 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGGLP 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 IQGMGFTAIWITPVTANL-EDGQHGEAYHGYWQQDIYALNPHFGTQDDLRALSDALHDRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 IQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 MYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 SLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 LQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDY
                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.

Boase N.A., Murphy R.M., Kelly J.M.;

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

EMBL, AF208225; AFR7103.1;

HSSP; P10529; 7TAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.0%; Score 1826; DB 2; Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1e-118;
53; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54249 MW; A891C4ACEAEB5305 CRC64;
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004556; F:alpha-amylase activity; IEA. GO; GO:0005975; P:carbohydrate metabolism; IEA. InterPro; IPR006047; Alpha amyl cat. InterPro; IPR006089; Alpha mmyl cat. InterPro; IPR006089; Alpha mmyl cat. InterPro; IPR006046; Glyco hydro. IPP00128; Alpha-amylase; I. PR00118; Alpha-amylase; I. PRINTS; PR00110; Alpha-Amylase;
                                                                                                                                                                                      490 AA
                                                                                                                                                                                                                                                                                                 Emericella nidulans (Aspergillus nidulans)
                                                                                                                                                                                                                     Created)
                                                                                                                                                                                      PRT;
                                                                             RVLYPTEKLAGSKIC 495
                                                                                           482 RVLYPTEKLAGSKIC 496
                                                                                                                                                                                                                  01-MAY 2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAX-2004 (TrEMBLrel. 26, Alpha-amylase AmyA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.68;
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                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00642; Aamy;
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                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                 metabolism; Glycoprotein; Glycosidase;
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                                                                                                                                                                                                                                                                                                                                                                                                        Production (by binariatity).

By similarity.

Calcium 1 (By similarity).

Calcium 1 (via carbonyl oxygen) (B similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

Calcium 1 (via carbonyl oxygen) (B similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

By similarity.

By similarity.
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0
at high concentrations (By similarity). SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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                                                                                                                                                                                                                                                                                                                                                               Alpha-amylase A.
Nucleophile (By similarity).
Proton donor (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 99.2%; Score 2662; DB 1; 11 Similarity 99.6%; Pred. No. 6.9e-177; 493; Conservative 0; Mismatches 2;
                                                                                                                                                                                                HSSP, P10529, 7TAA.

InterPro; IPR005699; Alp amyl_cat_sub.
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PP00118; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SWART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism Hydrolase; Multigene family; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54880 MW;
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TAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVD 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 NPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSE 377
                                                                                            SYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSS
    LYKLIASANAIRNYAISKDTGFVTYKWWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 ALGLSAAEWRSQSIYFLLTDRFGRTDNSTTATCDTGDQIYCGGSWQGIINHLDYIQGMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDCPYQDYLDGVLNYPIYWQLLYAFESSSGSISDLYNMIKSVASDCSDPTLLGNFIENHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIKDVVKANEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
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EMBL; AB081162; BAD06005.1; -.

EMBL; AB083160; BAD06003.1; -.

HSSP; P04064; IACZ.

GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0003875; P:catalytic activity; IEA.

GO; GO:0005975; P:catalytic activity; IEA.

InterPro; IPR006647; Alpha amyl cat.

InterPro; IPR006647; Alpha amyl cat.

InterPro; IPR00589; Alpha amyl cat.

InterPro; IPR002644; Glyco_hydro_CBD.

Pfam; PF00128; Alpha-amylase; 1.

Pfam; PF00188; GBM 20; 1.

Probom; PF001568; GBM 20; 1.
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634 AA; 69242 MW; 16C0BE6AF6FB0E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 1791; DB 2;
68.6%; Pred. No. 3.9e-116;
ive 64; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                634 AA
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 68.69
Matches 321; Conservative
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-amylase precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus awamori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=105351;
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Matsubara T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                        Acid-stable alpha-amylase.

Appergillus kawachi (Aspergillus awamori var. kawachi).

Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaneko A., Sudo S., Sakamoto Y., Tamura G., Ishikawa T., Ohba T.; "Molecular-cloning and determination of the nucleotide-sequence of gene encoding an acid-stable alpha-amylase from Aspergillus-kawachii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Kaneko A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, ABOOR910; BAA22993.1; -.
R HSSP; PS6271; ZAAA.
GO; GO:0003824; F:alpha-amylase activity; IEA.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0005975; P:catalytic activity; IEA.
R GO; GO:0005975; P:catalytic activity; IEA.
R GO; GO:0005975; P:catalytic activity; IEA.
R InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
R InterPro; IPR006044; Glyco hydro_CBD.
R Ffam; PF00128; Alpha-amylase; 1.
R Ffam; PF00686; CBM ZO; 1.
R Probom; PD001568; Glyco hydro_CBD; 1.
SWART; SW00642; Aamy; 1.
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                                                                                                                                                                                                                                                                    TJAN-1998 (TrEMBLrel. 05, Created)
1-JAN-1998 (TrEMBLrel. 05, Lást sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.4%; Score 1810; DB 2; 67.6%; Pred. No. 1.9e-117;
                                                                                                                                                                                                                                A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Ferment. Bioeng. 81:292-298(1996)
                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                  492 SKIC 495
                                                                                                            SGIC 488
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01-JAN-1998
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52935 MW; 04D596E34680656D CRC64;
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  484 AA;
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
 NAME INVESTIGES AND STROMS).

RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).

RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).

RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).

RAY MEDINE=910514; PubNed=2207069;

RAY Jensen V.J., Petersen S.B., Swift H., Thim L., Woldike H.F.;

RAY CRYCTC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic

C. -!- CATALYTIC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic

C. -!- CATALYTIC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic

C. -!- CATALYTIC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic

C. -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory

C. -!- COFACTOR: Balongs to the glycosyl hydrolase 13 family.

C. -!- SUBUNIT: Monomer:

C. -!- SUBUNIT: Monomer:

C. -!- SUBUNIT: Monomer:

C. -!- SUBUNIT: Ronofost to the glycosyl hydrolase 13 family.

DR PBB; 2AAA; X-ray; @=1-484.

INTERPRO'S 1PRO06699; Alp amyl_cat_sub.

DR PBB; 2AAA; X-ray; @=1-484.

INTERPRO'S 1PRO06699; Alp amyl_cat_sub.

DR PRO0642; Amyl; 1.

RW Glycosidase; Hydrolase.

FY ACT_SITE 200 Proton donor.

FY ACT_SITE 207 207 Calcium 1.

FY METAL 162 Calcium 1.

FY METAL 175 CALCIUM 2.

FY METAL 175 CALCIUM 2.

FY METAL 175 CALCIUM 1.

FY METAL 175 CALCIUM 1.

FY METAL 175 CALCIUM 2.

FY METAL 175 CALCIUM 1.

FY 
LYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGD 437
                                         P56271;
15-070-1998 (Rel. 36, Created)
15-070-1998 (Rel. 36, Last sequence update)
25-007-2004 (Rel. 45, Last annotation update)
Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
Aspergilus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium 1.
Calcium 1 (via carbonyl oxygen).
Calcium 1.
Calcium 2.
Calcium 1 (via carbonyl oxygen).
Calcium 2.
                                                                    SYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYP 485
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N-linked
N-linked
                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                              310 NFIENHDNPRFPNYTPDMSRAKAVTAPLTDGIPIVYAGGEQHYSGSNDPYNREPVWWS 369
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                                                                                                                        190 VSLTDLNTQSSEVRDIWYDWIEDIVANYSVDGLRIDTVKHVEKDFWPGYIDAAGVYSVGE
                                             VLDGDPAYTCPYQNVMDGVLNYP1YYPLLNAFKSTSGSMDDLYNM1NTVKSDCPDSTLLG
                         LQVAAPALAATPAD-WRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLD
                                                                                                  YIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHER
                                                                                                                                                                                                                                                      VSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGE
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Saccharomycetales, Lipomycetaceae, Lipomyces.
NCBI_TaxID=29829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and expression of Lipomyces starkeyi alpha-amylase in Escherichia coli and determination of some of its properties."; FEMS Microbiol. Lett. 233:53-64(2004). EMBL, AXIS5463; AAN/55021.1; -- HSSP; P26827; 1A47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=KSM 22M;
PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
Moon T.-W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 647;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1662; DB 2;
Pred. No. 3.8e-107;
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GO; GO:0005975; P:arbohydrate metabolism; IEA.
InterPro: IPR006047; Alpha_amyl_cat.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR005036; CBM_21.
Pfam; PF00128; Alpha-amylase; 1.
Pfam; PF00128; Alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
SMGUGUCE 647 AA; 70957 MW; D946071DB7560144
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61.4%;
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GSGLC 494
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                                                                              4 ASWRIQSIYFLLTDRFGRIDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAIWIS 63
                                                         24 ADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 TINAIRKLAIAADSAYITYANDAFYIDSNIIAMAKGISGSQVITVLSNKGSSGSSYTLIL
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                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boase N.A., Murphy R.L., Kelly J.M.;

Boase N.A., Murphy R.L., Kelly J.M.;

L. Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-- SIMILARIYTY Belongs to family 13 of glycosyl hydrolases.

R. EMBL; AF208224; AAF17100.1;

R. HSSP; P56771; ZAAA.

GO; GO:0004556; P:alpha-amylase activity; IEA.

R. GO; GO:000354; F:catalytic activity; IEA.

R. GO; GO:0005975; P:catbohydrate metabolism; IEA.

R. InterPro; IPR006689; Alpha_amyl_cat.

R. InterPro; IPR006689; Alpha_amyl_cat.

R. InterPro; IPR005094; GlyCo_hydro_IS.

R. InterPro; IPR005094; GlyCo_hydro_IS.

R. Pfam; PF00488; Alpha—amylase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name-amyB;
Emericella nidulans (Aspergillus nidulans).
Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                       Indels
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Last annotation update)
                       94;
   Pred. No. 2.2e-115;
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                   63; Mismatches
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ProDom; PD001568; Glyco_hydro_CBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
66.98;
                   Matches 318; Conservative
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   Best Local Similarity
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
                                                                                                                                                   ... amyl_cat_sub.
pha_amyl_cat.
1_21.
                                                                                                                            EMBL; U30376; AAC49622.1; ALT_INIT.
                                                                                                                                                         InterPro; IPR006589; Alp amyl_
InterPro; IPR006047; Alpha_amy
InterPro; IPR005036; CBM_21
                                                                                                                                                                                                                                                                                                                                                                                                                                       68876 MW;
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                                                                    FDGDPSYTCPYQENLDGVLAYPVYYPVVSAFESVSGSVSSLVDMIDTLKSECTDTTLLGS
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                                                                                                                                      SLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steyn A.J.C., Pretorius I.S.;
"Characterization of a novel alpha-amylase from Lipomyces kononenkoae and expression of its gene (LRA1) in Saccharomyces cerevisiae.";
Curr. Genet. 28:526-533 (1955).
-!-CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
                   LQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDY
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=IGC4052B;
MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA
gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Lipomycetaceae, Lipomyces.
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10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase 1 precursor (BC 3.2.1.1) (1,4-alpha-D-glucan)
Name=LKA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steyn A.J.C., Marmur J., Pretorius I.S.;
"Cloning, sequence analysis and expression in yeasts of a containing a Lipomyces kononenkoae alpha-amylase-encoding Gene 166:65-71(1995).
 Indels
 Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96132108; PubMed=8593683;
 75;
 Conservative
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Q01117;
10-OCT-2003 (
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Calcium 1 (By similarity).
Calcium 1 (By similarity).
Calcium 1 (Via carbonyl oxygen) (By similarity).
Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (Via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
By similarity.
By similarity. (B (By . 0 Length 624; Alpha-amylase 1. Carbohydrate binding type-21 Nucleophile (By similarity). Proton donor (By similarity) Indels 87EB16534F5A9A9F CRC64; ; Score 1629; DB 1; ; Pred. No. 7.1e-105; 77; Mismatches 113; •• Pfam; PF00128; Alpha-amylase; 1.
Pfam; PF03370; CBM\_21; 1.
SMART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Dis Glycoprotein; Glycosidase; Hydrolase; Signal SIGNAL

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        Qy
        375 DSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGA 434

        Db
        502 TSTFYEYIASINQIRNHAIYIDDTYLTYQNWVIYSDSTTIAMRKGFTGNQIITVLSNLGS 561

        Qy
        435 SGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKI 494

        Db
        562 SGSSYTLTLSNTGYTASSVVYEILTCTAVTVDLSGNLAVPMSGGLPRVFYPESQLVGSGI 621

        Qy
        495 CS

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        496

        Db
        622 CS

        Search completed: November 7, 2005, 18:52:29

        Job time: 269.266 secs
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7, 2005, 17:47:24; Search time 74.9884 Seconds (without alignments) 495.746 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		ULT 1  OB-720-899-7  equence 7, Application US/08720899  equence 7, Application US/08720899  equence 7, Application US/08720899  equence 7, Application US/08720899  aPPLICANT: Bisgaard-Frantzen, Hen  APPLICANT: Svendeen, Allan  APPLICANT: Thellersen, Marianne  APPLICANT: Van der Zee, Pia  TITLE OF INVENTION: AMYLASE VARIA  NUMBER OF SEQUENCES: 38  CORRESPONDENCE ADDRESS: ADDRESSE: No. 57534600 No. 575  STRET: New York  COUNTRY: USA  ZIP: 10174-6401  COMPUTER READABLE FORM: COMPUTER: BA FC COMPATION: COMPUTER: PLOST NO. 675  STATE: New York  COMPUTER: BA PC COMPATION: COMPUTER: PLOST NO. 675  STATE: New York  COMPUTER: DO. COMPATION: COMPUTER: PLOST NO. 675  STATE: New YOR  COMPUTER: DO. COMPATION: APPLICATION NUMBER: US/08/720,8  FILING DATE: 10-OCT-1996  CLASSIFICATION NUMBER: US/08/3,8  FILING DATE: 12-00-123  TELEPRAY: 212-807-9655  INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 478 amino acids  TYPE: amino acid STRANDEDNESS: single	
И 4 □ И 4 □ 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		plication US/0872, 3460 MATION: Bisgaard-Frantze: Borchert, Torben Svendsen, Allan Svendsen, Allan Van der Zee, Pia VENTION: AMYLASE EQUENCES: 38 NCE ADDRESS: NO. 57534600 M 405 Lexington Avei W York ew York Ew York Ew York ON OWERES: SYSTEM: PC-DOS/1 PRESET DEPPY disk FIE POPPY disk FIE POPPY disk TTS: 10-CT-1996 SYSTEM: PC-DOS/1 PRESET US/08 ON NUMBER: US 08 ON NUMBER: 31,2 CATION DATA: ON NUMBER: 31,2 CATION DATA: ON NUMBER: 31,2 CATION INFORMATION: TR: 10-CT-1996 TR: 10-CT-1996 ATION: AND	80 80 15 45 15 45
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		T. 1  UBEAL INFORMATION: WUERAL INFORMATION: WUERAL INFORMATION: APPLICANT: Bisgaard-Frant APPLICANT: Bisgaard-Frant APPLICANT: Bisgaard-Frant APPLICANT: Thellersen, Ma APPLICANT: Thellersen, Ma APPLICANT: Thellersen, Ma APPLICANT: Van der Zee, P TITLE OF INVENTION: AWILA NUMBER OF SEQUENCES: 38 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 57534600 STREET: New York STATE: New York COUNTRY: USA ZIP: 10174-6401 COMPUTER READABLE FORM: WEDIUM TYPE: FIDEPY dis COMPUTER: PECOMPUT COMPUTER: PO-DO SOFTWARE: PARENTION REDIUGATION: UNSHER: US FILING DATE: 10-CT-199 CLASSIFICATION DATA: APPLICATION NUMBER: US FILING DATE: 22-00-199 CLASSIFICATION NUMBER: 31 RELECOMMUNICATION NUMBER: 31 RELECOMMUNICATION NUMBER: 31 TELECOMMUNICATION NUMBER: 31 TELERAX: 212-867-0123 TELERAX: 212-867-0123 TELERAX: 212-867-0123 TELERAX: 212-878-9655 SEQUENCE CHARACTERISTICS: LENGTH: 478 amino acids TYPE: amino acids	ch al Simila 477; Cc
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00000000000000000000000000000000000000		ULT 1  08-720-899-7  atent No. 5753460  GENERAL INPORMATION:  APPLICANT: Bisgaard-Frantz  APPLICANT: Svendeen, Allan  APPLICANT: Svendeen, Allan  APPLICANT: Thellersen, Mar  APPLICANT: Thellersen, Mar  APPLICANT: Van der Zee, Pi  TITLE OF INVENTION: ANYLAS  NUMBER OF SEQUENCES: 38  CORRESPONDENCE ADDRESS:  ADDRESSEE: No. 57534600  STREET: New York  COUNTRY: USA  ZIP: 10174-6401  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: BM FC COMPATION: OF STATE: New York  COMPUTER: BM PC COMPATION: APPLICATION NUMBER: US/O  SOFTWARE: PACHATION OF STATE:  APPLICATION NUMBER: US/O  FILING DATE: 10-OCT-1996  CLASSIFICATION NUMBER: US/O  PRIOR APPLICATION DATA:  APPLICATION NUMBER: US/O  FILING DATE: 12-007-1994  ATTORNEY/AGENT INFORMATION:  REFERENCE/DOCKET NUMBER: 31  TELEFPHONE: 212-807-10123  TELEFPHONE: 212-807-0123  TELEFPHONE: 212-807-0123  TELEFPKX: 212-807-0123  TELENGTH: 478 amino acida  STARANDEDNESS: single	Query Ma Best Loc Matches
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		RESULT 1  US-08-720-899-7  US-08-720-899-7  Sequence 7, Application US/087208; Patent No. 5753460  GENERAL INFORMATION: APPLICANT: Bisgaard-Frantzen, APPLICANT: Svendeen, Allan APPLICANT: Van der Zee, Pia TITLE OF INVENTION: AMYLASE US NUMBER OF SEQUENCES: 38  CORRESPONDENCE ADDRESS: ADDRESSE: No. 57534600 No. 5TREET: 405 Lexington Avenuc CITY: New York STATE: New York CUNTYR: USA ZIP: 10174-6401  COMPUTER READABLE FORM: MEDIUM TYPE: Flopy disk COMPUTER: IBM PC COMPATION SOFTWARE: 10-0CT-1996 CLASSIFICATION NUMBER: US/08/7; PILING DATE: 20-NOV-1994 ATTORNEY/AGENT INFORMATION: NAME: LOWAD NUMBER: 406 FILING DATE: 22-NOV-1994 ATTORNEY/AGENT INFORMATION: NAME: LOWAD NUMBER: 406 FILING DATE: 22-807-9123 TELEPRAN: 212-807-9123 TELEPRAN: 212-807-9123 TELEPRAN: 212-807-9123 TELEPRAN: 212-807-9123 TELERAR: ATTORNEY ATT	<b>У</b> ш д

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Query Match 95.8
Best Local Similarity 99.8
Matches 477; Conservative
                                   ; STRANDEDNESS: sir; TOPOLOGY: linear US-08-459-610-7
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                     1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
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ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADOKYCGGTWOG11DKLDY1OGMGFTA1
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ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-UWN-1995
CLASSIFICATION: 435
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APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY Dr., Karen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08459610
Patent No. 5801043
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REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION: 212-867-0123
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pla
APPLICANT: Van der Zee, Pla
TITLE OF INVENTION: AMYLASE VARIANTS
CORRESPONDENCE 38
CORRESPONDENCE 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58308370 No. 5830837th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                     9
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COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPDY disk
COMPUTER: IBM PC compatible
COMPUTER: DATEMING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,804
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY Dr., Karen A.
                                                                                                                                                                       Score 2572; DB 1;
Pred. No. 3.2e-220;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 7, Application US/08343804; Patent No. 5830837; GENERAL INFORMATION:
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US-VG-DG3-DG4-LU
Sequence 10, Application US/08683838A
SEQUENCE INFORMATION:
SEQUENCES 10, Application Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
SADDRESSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
STREET: A05 Lexington Avenue, 64th Floor
STREET: New York
STATE: New York
STATE: New York
STATE: Now York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.8%; Score 2572; DB 2;
99.8%; Pred. No. 3.2e-220;
iive 0; Mismatches 1;
                                                                                                                                                                4394.204-US
UMBER: US/08/600,908A
13-FEB-1996
                                                                   CLASSIFICATION: 4.3.5
ATTORNEY/AGENT INFORMATION:
NAME: GREEN, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.8
Matches 477; Conservative
                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                FILING DATE: 13
CLASSIFICATION:
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US-08-683-838A-10
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Sequence 10, Sp8169

BATELIAND SEQUENCES:

APPLICANT: Svendeen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Bisg rd-Frantzen, Namylase Mutants
NUMBER OF SEQUENCES: 13
CORRESSONDERSS:
CORRESSONDERSS:
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER: RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
CORPUTER: BM PC compatible
CORPUTER: PLOSPY disk
CORPUTER: PLOSPY SYTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIR Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 PYQNVMDGVLAYYPLYYPLLANAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
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95.8%; Score 2572; DB 2;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1;
REGISTRATION NUMBER: 31,274
REPERENCE/DOCKET NUMBER: 4054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE: CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-343-804-7
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US-08-600-908A-10
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Pred. No. 3.2e-220;
0; Mismatches 1; Indels
             MEDIUW TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTONNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REBERENCE/DOCKET NUMBER: 38,475
RELEFAN: 212-867-0123
TELEPHONE: 212-867-0123
TELEFAN: 212-867-0123
TELEFAN: 212-87-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.8%;
Best Local Similarity 99.8%;
Matches 477; Conservative
COMPUTER READABLE FORM:
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US-09-182-859-7
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Patent No. 6143708
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik

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81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
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                FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-04-30
EARLIER FILING DATE: 1996-07-19
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 7
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APPLICANT: Svendeen, Torben
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutante
FILE REFERENCE: 4796.204.US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR PILING DATE: 1996-04-30
INVENTION: Alpha-Amylase Mutants
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Patent No. 6436888
                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7
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Best Local Similarity 99.8
Matches 477; Conservative
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61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNNNYGTADDLKALSSALHERGMYLMVDVVA 120
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                                                                                          21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                 Gaps
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           Length 478;
                                                 Indela
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99.8%; Pred. No. 3.2e-220;
iive 0; Mismatches 1;
    Query Match 95.8%; Score 2572; DB 4; Best Local Similarity 99.8%; Pred. No. 3.2e-220; Matches 477; Conservative 0; Mismatches 1;
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GENERALI INFOGRATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben,
APPLICANT: Borchert, Torben,
APPLICANT: Blegard-Frantzen, Henrik
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION WUMBER: US/09/672,459
FRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR PLING DATE: 1996-04-30
PRIOR PLING DATE: 1996-04-30
PRIOR PLING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-38
PRIOR FILING DATE: 1996-01-1
PRIOR FILING DATE: 1996-01-1
SPRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PSECSED OF WINDOWS VERSION 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 7, Application US/10186042; Patent No. 6642044; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.8
Matches 477; Conservative
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US-10-186-042-7
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Pred. No. 3.2e-220;
0; Mismatches 1;
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APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/616,252A
CURRENT FILING DATE: 1996-07-18
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR PILING DATE: 1996-075/96
PRIOR PILING DATE: 1996-07-11
PRIOR PLING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR PLING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 7
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Sequence 10, Application US/09636252A
Patent No. 6440716
GENERAL INFORMATION:
                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7
                                                                                                                                                                                                                                                                                                       Vuery Match 95.8%;
Best Local Similarity 99.8%;
Matches 477; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: A. C
US-09-636-252A-10
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LENGTH: 478
TYPE: PRT
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Indels
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Pred. No. 4e-214;
1; Mismatches 8;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/08470702; Patent No. 5631149
TELEFAX: 202-824-8199
TELEX: 248516
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-715A-2
                                                                                                                                                                                                    93.3%;
                                          7
                                                                                                                                                                                                                     Best Local Similarity Autohes 468; Conservative
                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                               81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
                                                                                                                                                                                                                   61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
                                                                                                                                                                                                 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
                                                                                                                                                                                                                                                                      PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
                                                                                                                                                                                                                                                                                                                                          FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
                                                                                                                                                                                                                                                                                                                                                                  LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
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                                                                                                                          NEMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
   1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2. Application US/08339715A

Sequence 2. Application US/08339715A

Patent No. 596542

GENERAL INFORMATION:
APPLICANT: Kaneko, Hiroki
APPLICANT: Takada, Toshikazu
APPLICANT: Kuriki, Takashi
APPLICANT: Yanase, Michiyo
APPLICANT: Takata, Hiroki
APPLICANT: Takata, Hiroki
APPLICANT: Takata, Hiroki
APPLICANT: Takata, Hiroki
APPLICANT: NUNENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
ITTLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
CORRESPONDENCE ADDRESS:
ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,715A
FILLING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & STREET: Metropolitan Square Building, STREET: G. Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Melser, Allen S.
REGISTRATION UNDMER: 27,215
REFERENCE/DOCKET UNDMER: 18335.009
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
STATE: D.C.
COUNTRY: USA
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141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 FASYTNDIALAKAVAAFIILNDGLPIIYAGQEQHYAGGNDFANREATWLSGYPTDSELYK 360
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APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: HONDA, XOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE BNZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatchouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVVKNEWYDWVGSLVSNYSI DGLRI DTVKHVQKDFWPGYNKAAGVYCI GEVLDGDPAYTC
                                                                                                                                                                                                                                                         WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                   1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                           21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                  Gaps
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Length 478;
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141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
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VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
OLIGOSACCHARIDE USING THE ENZYME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 FASMTSDQSLISNAIAFVLLGDGIPVIYYGQEQGLSGKSDPNNREALWLSGYNKESDYYK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 INADKWRSQSIYQIVTDRFARTDGDTSASCNTEDRLYCGGSFQGIIKKLDYIKDMGFTAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 TPAD-WRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                  E: BIRCH, STEWART, KOLASCH & BIRCH
8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYRE: Floppy disk
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-JUN-1995
CLASSIPICATION: 435
RLOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISSTRATION NUMBER: 32,181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELERAX: (703) 205-8050
TELERAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 468 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: VAR
TITLE OF INVENTION: VAR
TITLE OF INVENTION: OLI
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                       STREET: 8110 Gatehou
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 WISPVVENIPDNTAYGYAYHGFWMKNIYKINENFGTADDLKSLAQELHDRDMLLMVDIVT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 PYQNYIPGVSNYPLYYPTTRFFKTTDSSSSELTQMISSVASSCSDPTLLTNFVENHDNER 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 468;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.9%; Score 1392; DB 1; Best Local Similarity 54.4%; Pred. No. 3.1e-115; Matches 259; Conservative 81; Mismatches 126;
                                   APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIPFICATION: 435
FRICA APPLICATION: 435
PRICA APPLICATION: 0ATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTONNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100-205-8000
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Patent No. 5655378
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAMA, KAZUHIKO
APPLICANT: HANNA, KAZUHIKO
APPLICANT: HONDA, KOICHI
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 468 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: "
                                                                                                                                                                                                                                                                                                                                           TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
242 PYQNYIPGVSNYPLYYPTTRFFKTTDSSSSELTQMISSVASSCSDPTLLTNFVENHDNER 301
                                                                             302 FASMTSDOSLISNAIAFVLLGDGIPVIYYGQEQGLSGKSDPNNREALWLSGYNKESDYYK 361
                                                                                                                     381 LIASANAIRNYAISKOTGFVTYKNWPIYKODTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08470702

Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: MISTRIA, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATUR SYTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.8%; Score 1391; DB 1;
54.4%; Pred. No. 3.8e-115;
iive 81; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWAKE: PAGENTIN Release #1.0, Verication Application Number: US/08/470,702
FILING DATE: 06-UNN-1995
CLASSIPICATION NUMBER: US/08/470,702
FILING DATE: 06-UNN-1995
CLASSIPICATION ATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656
FILING DATE: 02-MAR-1994
ATTOMNE: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELEPHONE: (703) 205-8000
TELERA: (703) 205-8000
TELERA: (703) 205-8000
TELERA: (703) 205-8050
TELERA: 248345
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 468 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 259;
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                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TNADKWRSQSIYQIVTDRFARTDGDTSASCNTEDRLYCGGSFQGIIKKLDYIKDMGFTAI 61
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                                     Length 468;
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COUNTRY: U.S. A.
ZID.
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54.4%; Pred. No. 3.8e-115;
cive 81; Mismatches 126;
                                                                                                                                                         Sequence 4, Application US/08204656B Patent No. 5538882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weller, Marc S.
REGISTRATION NUMBER: 32,181
REPERNCK/DOCKET NUMBER: 234-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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259; Conservative
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WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
                 NHMGYDGAGSSVDYSVPKPPSSQDYFHPPCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
                                                                            SDVASVENSWYKDFVGNYSIDGLRIDSAKHVDQGFFPDFVSASGVYSVGEVFQGDPAYTC 241
                                                                                                                                                                                 PYONVMDGVLNYPIYYPLILNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
                                                                                                                                                                                                 242 PYQNYIPGVSNYPLYYPTTRPPKTTDSSSSELTQMISSVASSCSDPTLLTNFVENHDNER 301
                                                                                                                                                                                                                                          PASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
                                                                                                                                                                                                                                                          LIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
                                                                                                                                                                                                                                                                                                                        APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAMA, KAZUHIKO
APPLICANT: MISHIRI, SACHIO
APPLICANT: MISHIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  496
                                                                                                                     201 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
PILING DATE: 06-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/204,656
FILING DATE: 02-WAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
RECECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08467831
Patent No. 5635378
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 205-8050
TELEEX: 248345
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 LSLSGAGYTAGOQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS
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                                                                                                                                                              Length 468;
                                                                                                                                                              Query Match 51.8%; Score 1391; DB 1; Best Local Similarity 54.4%; Pred. No. 3.8e-115; Matches 259; Conservative 81; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7, 2005, 18:25:06
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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APP-5, Appl 18, Appl 12469, A

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2223, Ap 22679, A 22723, A 291647,

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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Title: Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Minimum DB Maximum DB

Database

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61 TWQGIIDKLDYLQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120
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US-10-820-200-2
; Sequence 2, Application US/10820200
; Publication No. US20040229764A1
; GENERAL INFORMATION:
    APPLICANT: Biggard-Frantzen, Henrik
    APPLICANT: Pedersen, Sven
    APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; FILE REFERENCE: 5835.200-US
; CURRENT FILING DATE: 2004-04
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR APPLICATION NUMBER: US/09/710,339
; RIOR FILING DATE: 2000-11-09
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; LENGTH: 498
US-10-980-759-7

US-11-064-196-10

US-10-278-84-43

US-10-213-990-42

US-10-213-990-42

US-10-213-990-42

US-10-213-990-42

US-10-213-990-45

US-10-213-990-45

US-10-877-849-41

US-10-877-849-41

US-10-877-849-34

US-10-877-849-34

US-10-877-849-34

US-10-877-849-34

US-10-877-849-34

US-10-877-849-34

US-10-877-849-34

US-10-137-393-12469

US-10-369-493-2223

US-10-369-493-2223

US-10-369-493-2223

US-10-369-493-2223

US-10-369-493-2223

US-10-369-493-22723

US-10-369-493-19940

US-10-369-493-19940

US-10-369-493-19062

US-10-369-493-19062

US-10-369-493-19062

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US-10-425-115-291-447-447-448-900-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Aspergillus Oryzae
US-10-820-200-2
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Best Local S:
Matches 498
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Sequence 40,
Sequence 36,
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Sequence 22,
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Sequence 7,
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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US-10-877-849-40
US-10-877-849-40
US-10-817-849-36
US-10-815-495-18
US-10-815-495-12
US-10-815-495-22
US-10-815-495-22
US-10-815-495-22
US-10-644-187-7
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                  GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                          KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLINAFKSTSGSMDDLYNMINTVK
                                                                                                              SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
                                                                                          SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND
                                                                                                                                                              PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
                       KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10797393A
Publication No. US20040219649A1
GENERAL INFORMATION:
APPLICANT: Olsen, Hans Sejr
APPLICANT: Pedersen, Sven
TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
FILE REFERENCE: 10391.200-US
CURRENT APPLICATION NUMBER: US/10/797,393A
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 5
SSC ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Aspergillus oryzae
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Matches 498; Conservative
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US-10-797-393A-5
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APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Taira, Rihabu
APPLICANT: Aliain, Eric
APPLICANT: Aliain, Eric
APPLICANT: Hjort, Carsten
APPLICANT: Hjort, Carsten
APPLICANT: 10490-Nucleus
TITLE OF INVENTION: HYBRID BNZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490-500-US
CURRENT APPLICATION NUMBER: US/10/877,849
CURRENT APPLICATION NUMBER: US/10/877,849
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEQ ID NO 30
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US-10-877-849-30
Sequence 30, Application US/10877849
Publication No. US20050054071A1
GENERAL INFORMATION:
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; ORGANISM: Aspergillus oryzae
US-10-877-849-30
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                                                                                                                                                                         APPLICANT: Taira, Rikako,
APPLICANT: Taira, Rikako,
APPLICANT: Taira, Rikako,
APPLICANT: Allain, Eric
APPLICANT: Hjort, Carsten
APPLICANT: Hjort, Carsten
APPLICANT: Vikso-Nielsen, Anders
ITILE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490.500-1000
CURRENT APPLICATION NUMBER: US/10/877,849
CURRENT FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Version 3.2
SEQ ID NO 36
                                                                                             Sequence 36, Application US/10877849;
Publication No. US20050054071A1;
GENERAL INFORMATION:
APPLICANT: Udagawa, Hiroaki
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US-10-815-495-18
'S Sequence 18, Application US/10815495
'Publication No. US20040191864A1
481 RVLYPTEKLAGSKICSSS 498
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; OTHER INFORMATION: Artificial
US-10-877-849-36
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ORGANISM: Artificial
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                                                                                                                                                                                                                                  Sequence 40, Application US/10877849
Publication No. US2050054071A1
GENERAL INFORMATION:
APPLICANT: Udagaw, Hiroaki
APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Allain, Eric
APPLICANT: Hjort, Carsten
APPLICANT: Vikso-Nielsen, Anders
TILE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REFERRINCE: 10490.500-US
CURRENT APPLICATION WUMBER: US/10/877,849
CURRENT APPLICATION NOWBER: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOUTHARE: Patentin version 3.2
SEQ ID NO 40
LENGTH: 608
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; Pred. No. 3.5e
0; Mismatches
                                                                                             RVLYPTEKLAGSKICSSS 498
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Best Local Similarity 100.0%;
Matches 498; Conservative 0.
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; OTHER INFORMATION: Artificial
US-10-877-849-40
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US-10-877-849-40
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RVLYPTEKLAGSKIC 495
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          ; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22
                                                                                                Query Match
Best Local Similarity 99.6
Matches 493; Conservative
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; ORGANISM: A.
US-10-184-771-10
 SEQ ID NO 22
LENGTH: 498
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           APPLICANT: Novozywes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Matants Of Aspergillus Niger
TITLE OF INVENTION: Matants Of Aspergillus Niger
TITLE OF INVENTION: Matants Of Aspergillus Niger
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/10815495
Sequence 22, Application US/10815495
Publication No. US20040191864A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Matants Of Aspergillus Niger
FILE REFERENCE: 10345.200-US
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
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Pred. No. 1.8e-212;
0; Mismatches 2;
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                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.6
Matches 496; Conservative
GENERAL INFORMATION:
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US-10-815-495-22
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                                                                                                                                                                2 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
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         Length 498;
                                                                Indels
99.2%; Score 2662; DB 16;
99.6%; Pred. No. 1.8e-211;
tive 0; Mismatches 2;
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APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
FILE REFERENCE: 0776/1F216-U52
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PSELSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 478
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; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
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380

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PYQNVMDGVLNYPIYYBLLANAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
                                                                   61 WITPVTAQLPQTTAYGDAYHGYWQQDIXSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
                                                                                                                                                                                                                        DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQXDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
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                                                                                                                                                            121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
                                                                                                                                    141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
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  1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                              81 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
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US-10-644-18/-7

Publication No. US20040048351A1

GENERAL INFORMATION:

APPLICANT: Svendeen, Allan

APPLICANT: Bisgard-Frantzen, Henrik

TILE REPERBNCE: 4796.204-US

CURRENT APPLICATION NUMBER: US/10/644,187

CURRENT FILING DATE: 2003-08-20

PRIOR APPLICATION NUMBER: 05/182,859

PRIOR PELING DATE: 1996-0-29

PRIOR PELING DATE: 1996-04-30

PRIOR PELING DATE: 1996-04-30

PRIOR PILING DATE: 1996-07-11

PRIOR PILING DATE: 1996-11-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PSEXERO FOR WINGONE VETSION 3.0
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Best Local Similarity 99.8'
Matches 477; Conservative
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                                                                   1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIDDKLDYIQGMGFTAI
                                            21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10186042
| Publication No. US20030171236A1
| GENERAL INFORMATION:
| APPLICANT: Svendeen, Allan
| APPLICANT: Svendeen, Allan
| APPLICANT: Bisgard-Frantzen, Henrik
| APPLICANT: Bisgard-Frantzen, Henrik
| FILE REFERENCE: 4796.204-US
| CURRENT APPLICATION NUMBER: US/10/186,042
| CURRENT APPLICATION NUMBER: US/09/672,459
| PRIOR APPLICATION NUMBER: US/09/672,459
| PRIOR PILING DATE: 2000-09-28
| PRIOR APPLICATION NUMBER: 03/182,859
| PRIOR PILING DATE: 1998-10-29
| PRIOR PILING DATE: 1998-10-29
| PRIOR PILING DATE: 1996-04-30
| PRIOR PILING DATE: 1996-07-11
| PRIOR PILING DATE: 1996-11-08
| WINGHER OF SEQ ID NOS: 37
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477; Conservative
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LENGTH: 478
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Pred. No. 4.7e-204;
0; Mismatches 1;
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APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
APLICANT: Bisgard-Frantzen, Henrik
APLICANT: Bisgard-Frantzen, Henrik
TTILE APLICATION: Alpha-Amylase Mutants
FILE REFERENCE: 4795.204.03
CURRENT APPLICATION NUMBER: US/09/672,459
RRIOR APPLICATION NUMBER: US/09/672,459
RRIOR FILING DATE: 1090-029
RRIOR FILING DATE: 1996-10-29
RRIOR APPLICATION NUMBER: 0515/96
RRIOR APPLICATION NUMBER: 0715/96
RRIOR APPLICATION NUMBER: 0715/96
RRIOR FILING DATE: 1996-06-28
RRIOR FILING DATE: 1996-06-28
RRIOR FILING DATE: 1996-07-11
RRIOR FILING DATE: 1996-07-11
RRIOR APPLICATION NUMBER: 1263/96
RRIOR FILING DATE: 1996-07-11
RRIOR FILING DATE: 1996-07-11
RRIOR FILING DATE: 1996-07-11
RRIOR FILING DATE: 1996-07-11
Mismatches
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Best Local Similarity 99.8%;
Matches 477; Conservative 0
Conservative
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                        NHWGYDGAGSSVDYSVFKPPSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 180
                                                                                                        DVVKNEWYDFWYGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 240
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                                                                                                                                                                                         PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
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                                                                                 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
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STATE: New York
COUNTRY: United States of America
ZIP: 1014-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CONPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/926,720
FILING DATE: 26-Aug-2004
CLASSIFICATION: CURKNOW>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/10926720
Publication No. US2005019866A1
GENERAL INFORMATION:
APPLICANT: Svendeen, Allan
Bigg+rd-Frantzen, Henrik
Bigg+rd-Frantzen, Henrik
Derchert, Torben Vedel
TITLE OF INVENTION: -Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.8%; Score 2572; DB 17; 99.8%; Pred. No. 4.7e-204;
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REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
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Best Local Similarity
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US-10-926-720-10
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301 FASYTNDIALAKAVAAFIILNDGIPIIYAGQEQHYAGGNDFANREATWLSGYPTDSELYK 360
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                                                            241 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
                                                                                                               PASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
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 DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 240
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43. Application US/10877849

Publication No. US200S0054071A1

GENERAL INFORMATION:
APPLICANT: Udagawa, Hiroaki
APPLICANT: Taira, Rikako
APPLICANT: Taira, Shinobu
APPLICANT: Taira, Shinobu
APPLICANT: Taira, Shinobu
APPLICANT: Hjort, Carsten
APPLICANT: Vikso-Nielsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490.500-US
CURRENT APPLICATION NUMBER: US/10/877,849
CURRENT FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEQ ID NO 43
LENGTH: 476
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ORGANISM: Aspergillus oryzae
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; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43
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                                                                                                                                                                                                        LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYT 440
                                                            61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
                                                                                                                                                                                     DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
                                                                                                                                                                                                                                                                                 301 FASYTNDIALAKAVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPIDSELYK 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/11064196
Publication No. US20050170487A1
GENERAL INFORMATION:
APPLICANT: Svendeen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TILB OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/11/064,196
CURRENT APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1996-07-18
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FeatSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: A. Oryzae
US-11-064-196-10
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                61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
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Best Local Similarity 99.8%; Pred. No. 2.7e-203;
Matches 477; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                   RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. USZ0030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: SAlf-processing Plants and Plant Parts
; FILE REFERENCE: 109846,317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; UNRBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                         LENGTH: 1095
7 TYPE: PRT
ORGANISM: Aspergillus shirousami
US-10-228-063-45
 381
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Search completed: November 7, 2005, 18:45:02 Job time: 274.151 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 7, 2005, 18:40:32; Search time 1.50579 Seconds

(without alignments)

830.671 Million cell updates/sec
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Title:

Perfect score:
78
Sequence:
1 AYHGYWQDDIYSL 13
Scoring table:
Gapop 10.0 , Gapext 0.5
Searched:
283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:\* 1: Dirl:\* 2: Dir2:\* 3: Dir3:\* 4: Dir4:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		A48305	ALAS1	ALAS3	JS0663	JT0466	JN0588	B48305	T38770	S72270	A35282	833921	JK0201	JC4510	S31478	ALBYAF	T40860	T38448	T41503	862505	S23355	806115	T41603	ALBSK	B82409	ALBSG3	ALBSG7	ALBSG1	ALBSXR	A58800
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	Score	78	78	78	78	78	78	78	67	99	64	64	62	62	29	58	26	54	23	25	20	20	20	49	49	49	49	49	49	49
	Result No.	7	7	٣	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

cyclomaltodextrin cyclomaltodextrin	cyclomaltodextrin cyclomaltodextrin glycosyl hydrolase	<pre>cyclomaltodextrin cyclomaltodextrin cyclomaltodextrin</pre>	cyclomaltodextrin cyclomaltodextrin cyclomaltodextrin	alpha-amylase (EC alpha-amylase (EC alpha-amylase (imp	alpha-amylase (imp alpha-amylase (EC
S09196 ALBSG6	ALBSGC ALBSMX G75392	ALKBG ALBSX1 I3980S	S63598 ALBSXF ALBSGR	S28784 AH0979 F91185	D86032 S23807
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713	718 718 483	655 703 704	710	717 675 676	676 676
62.8	62.8 60.3	59.0 59.0	59.0 59.0 59.0	57.7 56.4 56.4	56.4 56.4
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30	3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	36 37 37	38 40 40	4 4 4 13 2 3	44 45

## ALIGNMENTS

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A48305
alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe
A;Reference number: A48305
A;Reference number: A48305
A;Reference number: A48305
A;Residues: preliminary; not compared with conceptual translation
A;Residues: UNIPROT:Q02905
A;Residues: 1-498 «KOR»
A;Residues: UNIPROT:Q02905
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/stach degradation
C;Superfamily: Aspergillus alpha-amylase; polysaccharide degradation
C;Superfamily: Aspergillus alpha-amylase; polysaccharide degradation
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide service homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
C;Keywords: glycoprotein; glycosidase; hydrolase; glycoprotein; glycopr
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## LT 2 1 a emylase (BC 3.2.1.1) 1 precursor [validated] - Aspe ternate names: alpha-amylase isozyme II; glycogenase;

Alternate amylase (EC 3.2.1.1) I precursor [validated] - Aspergillus oryzae
N;Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
C;Species Aspergillus oryzae
C;Species Aspergillus oryzae
C;Species Sepergillus oryzae
C;Species So-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C;Accession: S04548; A33214; J898
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon A;Reference number: S04548; MUID:89237897; PMID:2785629
A;Accession: S04548
A;Accession: S04548
A;Residues: 1-499 cWIR>
A;Residues: 1-499 cWIR>
A;Genetics: AMYI
A;Residues: 1-499 cWIR>
A;Genetics: AMYI
A;Residues: 1-499 cWIR>
A;Molecule type: mRNA
A;Residues: 1-499 cWIR>
A;Cross-references: GB:X12725; NID:92430; PIDN:GAA31218.1; PID:9295921
B;Genes, M.J.; Dove, M.J.; Seligy, V.L.

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1 AYHGYWQQDIYSL 13
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Altitle: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing A; Fatterence number: J80240; MUD:89378767; PMID:2789162
A; Reference number: J80240
A; Rolecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-499 <GEN>
A; Residues: 1-499 <GEN>
A; Residues: 1-499 <GEN>
A; Residues: 1-490 <GEN>
A; Residues: 3.; Richarka, T.
J. Biochem. 74, 1-10, 1973
A; Reference number: A91930; MUD:74001521; PMID:4733850
A; Recession: A91930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.penacription: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A.pathway: glycogen/starch degradation
A.pathway: glycogen/starch degradation
C.Superfamally: Asperglilus alpha-amylase core homology
C.Superfamally: Asperglilus alpha-amylase in glycoprotein; glycosidase; hydrolase; polys
C.Superfamally: Asperglilus alpha-amylase; predicted <SIG>
F.1-21/Domain: signal sequence #status predicted <SIG>
F.1-21/Domain: alpha-amylase core homology <AMY>
F.194-321/Domain: alpha-amylase core homology <AMY>
F.51-59.171-185,261-304,461-496/Disulfide bonds: #status experimental
F.142.183.196,231/Bindhing site: calcium (Asn, Glu, Asp, His) #status predicted
F.218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F.218/Sinding site: carbohydrate (Asn) (covalent) #status experimental
F.227,251,318/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Reference number: A93167
A.Accession: A93767
A.Accession: A. Kusunoki, M.; Harada, W.; Kakudo, M.
B.Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
B.Matsuura, Y.; Kusunoki, M.; Harada, M.; Kakudo, M.
A.Fitle: Structure and possible catalytic residues of Taka-amylase A.
A.Reference number: A37454; MUID:84212370; PMID:660921
A.Reference number: A37454; MUID:84212370; PMID:660921
A.Fishift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkenburg, J.P.; Wilkinson, A.
submitted to the Brookhaven Protein Data Bank, August 1992
A.Accestion number: A51548; PDB:67AA
A.Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497
C.Comment: One atom of calcium per molecule is essential for activity.
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N.Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: 804549; A33215; A44713
R;Mirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Ittle: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon (A;Reference number: S04548; MUID:89237897; PMID:2785629
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Pred. No. 4.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Genetics: <AMY2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Jpn. Acad. 51, 285-290, 1975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 206-225 <ISE>
R,Narita, K.
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Best Local Similarity
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A; Residues: 1-499 <WIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: amy2; AmyII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics: <AMY1>
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A, Cross-references: UNIPROT: Q96TH4; EMBL: X12727; NID: 92454; PIDN: CAA31220.1; PID: 9295922

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A;Status: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-499 < MIZ.>
A;Eesidues: 1-499 < MIZ.>
A;Cross.references: GB:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
B;Genes, M.J.; Dove, M.J.; Seligy, V.L.
R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
A;Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing A;Reference number: J$0240; MUID:89378767; PMID:2789162
A;Accession: A44713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; meta
F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 22-499/Product: alpha-amylase 3 #status experimental <AMT>
F; 194-321/Domain: alpha-amylase core homology <AMY>
F; 195-59, 171-185, 261-304, 461-496/Disulfide bonds: #status experimental
F; 142, 183, 196, 231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F; 21, 251, 318/Active site: His, Glu, Asp #status experimental
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RyShibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expression.
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A; Residues: 1-499 <SHI>
C; Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase; hydrolase; polysaccharide degradation
F;121/Domain: signal sequence #status predicted <SIG>
F;124-91/Product: alpha-amylase ecre homology <AMY>
F;124-150/Product: alpha-amylase core homology <AMY>
F;18/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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C;Species: Aspergillus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Structure and possible catalytic residues of Taka-amylase A. A,Reference number. A37454; MUD:84212370; PMUD:660921
A;Contents: annotation; X-ray crystallography, 3.0 angstroms C;Conment: One atom of calcium per molecule is essential for activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: amy3; Amy1
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 78; DB 2; I
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                         A, Residues: 1.499 <GEN>
A, Note: the authors refer to this as isozyme I
R, Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Blochem. 95, 697-702, 1984
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Matches 13; Conservative
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Cipecates: Aspergillus awamori
Cipecates: Aspergillus awamori
Cipace: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
Cipace: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
Cipacession: B4830s; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asp-A;Reference number: A48305; MulD:90254827; PMID:2340591
A;Accession: B48305
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-499 <KOR>
A;Residues: 1-499 <KOR>
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A;Cross-references: UNIPROT:014154; EMBL:298762; PIDN:CAB11471.1; GSPDB:GN00066; SPDB:S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Afforestreferences: UNIPROT:002906
C;Function:
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology
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C;Dete: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T89770
C;Sklton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, August 1997
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C;Species: Cryptococcus sp.
A;Variety: strain CS2
C;Date: 23-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
                      Gaps
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100.0%; Pred. No. 4.1e-05;
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Pred. No. 0.0027;
2; Mismatches 1
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A;Molecule type: DNA
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                   Mismatches
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1 Similarity 76.9%;
10; Conservative
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                                                                            1 AYHGYWQQDIYSL 13
            13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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A, Accession: T38770
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Best Local Similarity
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A;Gene: SPDB:SPAC4A8.01
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                                                                                                                                            alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N;Alternate names: glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JT0466
R;Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A;Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergill
A;Reference number: JT0466
A;Accession: JT0466
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R;Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kirita, N.; Tsuboi, A.; Udaka, S.
Gene 84, 319-327, 1989
A;Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for mu A;Reference number: JN0588; MUID:90128276; PMID:2612911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Figure, as a special property of internal 1,4-alpha-D-glucosidic bonds A; Pathway: glycogen/starch degradation
A; Pathway: glycogen/starch degradation
A; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-49/Product: alpha-amylase #status predicted <AMT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;194-321/Domain: alpha-amylase (Ash) (covalent) #status predicted
F;218/Binding site: carbohydrate (Ash) (covalent) #status predicted
F;231,251,318/Active site: His, Glu, Asp #status predicted
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Pathway: glycogen/starch degradation
;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology;
;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
;1-21/Domain: signal sequence #status predicted <SIG>
;124-99/Product: alpha-amylase #status predicted <MAT>
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N;Alternate names: Taka-amylase A
C;Species: Aspergillus oryzae
C;Pate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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A; Residues: 1-499 < TADD>
A; Residues: 1-499 < TADD>
A; Cross-references: UNIPROT: P10529
C; Comment: See also PTR: JK0201 and PIR: JS0240.
C; Comment: One atom of calcium per molecule is essential for activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred, No. 4.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
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A; Cross-references: UNIPROT: Q96TH4
C; Comment: The alpha amylases are encoded by multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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99 AYHGYWQQDIYSL 111
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Best Local Similarity
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A;Gene: Taa-G1
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Matches
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A;Cross_references: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g396: CGenetics: A;Gene: SWA2 C;Function:
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NyAlternate names: LKA1 protein; raw starch-degrading amylase
NyContains: alpha-dextrin endo-1,6-alpha-glucosidase (BC 3.2.1.41)
C;Species Lipomyces kononenkoae
C;Accession: JC4510; PC4116
C;Accession: JC4510; PC4116
C;Accession: JC4510; PC4116
A.A.G.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A;Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lip
                                                                                                                                                                                                                                    A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pesthway: glycogen/starch degradation C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation F;1-20/Domain: signal sequence #status predicted <SIG>F;21-507/Product: alpha-amylase #status predicted <MAT>F;21-507/Product: alpha-amylase core homology <AMY>F;205-312/Domain: alpha-amylase core homology <AMY>F;1-20/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;173-300/Domain: alpha-amylase core homology <AMY>
F;197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;210,230,297/Active site: His, Glu, Asp #status experimental
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N;Alternate names: glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Mar.1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JK0201
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C;Comment: One atom of calcium per molecule is essential for the activity.
C;Comment: This enzyme is a glycoprotein.
C;Comment: See also PIR:JT0466 and PIR:JS0240.
C;Function:
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Pred. No. 0.0084;
3; Mismatches 1; Indels
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Proc. Jpn. Acad. 58B, 208-212, 1982
A;Title: The complete amino acid sequence of Taka-amylase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.1%;
69.2%;
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Best Local Similarity 69.2.
Best Local 9; Conservative
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A; Accession: JK0201
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A;Molecule type: mRNA
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                                                               C;Accession: S72270

R;Iefuji, H; Chino, M; Kato, M.; Iimura, Y.
Biochem. J. 318, 989-996, 1996
A;Title: Raw-starch-digesting and thermostable alpha-amylase from the yeast Cryptococcus A;Title: Raw-starch-digesting and thermostable alpha-amylase from the yeast Cryptococcus A;Reference number: S72270; MUID:96433120; PMID:8836148
A;Reseidues: S72270; MUID:96433120; PMID:8836148
A;Residues: 1-611 <IRE>
A;Residues: 1-611 <IRE>
A;Residues: 1-631 <IRE
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C;Species: Aspergillus niger
C;Species: Aspergillus niger
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35282 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35282 #sequence_revision 10-Sep-1999
Biochemistry 29, 6244-6249, 1990
A;Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom r
A;Reference number: A35282 #MID:91002514; PMID:2207069
A;Accession: A35282
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Molecule type: mRNA
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N;Alternate names: alpha-1,4 glucanohydrolase
C;Species: Schwanniomyces occidentalis
C;Species: Schwanniomyces occidentalis
C;Accession: 333921
E;Clarcs, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
Curr. Genet. 24, 75-83, 1993
A;Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase in A.Reference number: S33921; MUID:99365041; PMID:8958835
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C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;173-300/Domain: alpha-amylase core homology <AMY>
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Pred. No. 0.008;
1; Mismatches
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Pred. No. 0.005;
1; Mismatches
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Matches 10; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                    A; percription: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages A; Pathway: glycogen/starch degradation c. Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch c. Superfamily: Lipomyces alpha-amylase; alpha-amylase starch c. Superfamily: Lipomyces alpha-amylase; alpha-amylase; polysaccharide F; 1-28/Domain: signal sequence #status predicted <MAT> F; 29-624/Product: alpha-amylase starch-binding domain homology <SBD> F; 48-141/Domain: alpha-amylase core homology <AMT> F; 320-447/Domain: alpha-amylase core homology <AMY> F; 177-185, 297-311, 387-430, 587-622/Disulfide bonds: #status predicted F; 370-44/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 377, 444/Active site: His, Glu, Asp #status predicted
Residues: 1-624 <STE>
| Gross-references: UNIPROT:Q01117; GB:U30376; NID:g1173536; PIDN:AAC49622.1; PID:g11735; Experimental source: strain IGC4052B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; H
submitted to the EMBL Data Library, December 1992
A;Description: The gene amyTV coding for a non-glucogenic alpha-amylase from Thermoactin
A;Reference number: S31478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Saccharomycopsis fibuligera
C;Species: 30-Unn-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S00064
R;Itoh, T.; Yamashita, I.; Fukui, S.
R;Itoh, T.; Yamashita, I.; Fukui, S.
A;Itile: Nucleoride sequence of the alpha-amylase gene (ALP1) in the yeast Saccharomycop A;Reference number: S00064; MUID:87276512; PMID:3497057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:g48289; PIDN:CAA49465.1; PID:g48290;
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A; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: glycosidase; hydrolase; polysacharide degradation
P;194-319/Domain: alpha-amylase core homology <AMY>
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S31478
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Pred. No. 0.022;
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Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                               A;Molecule type: protein
A;Residues: 29-44 <ST2>
A;Experimental source: IGC4052B
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Best Local 9; Conservative
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A,Residues: 1-482 <HOF>
A,Cross-references: UNIE
C,Function:
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A; Molecule type: DNA
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A; Residues: 1-494 <ITO>
A; Cross -references: UNIPROT: P21567; EMBL: X05791; NID: 94847; PIDN: CAA29233.1; PID: 94848
A; Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Th C; Genetics:
A; Genetics: ALPI
C; Function: Apple and a parachation of the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Th A; Genetics: ALPI
C; Function: A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: calcium; extracellular protein; glycoprotein; glycosidase; hydrolase; metal F; 1-26/Domain: alpha-amylase fatatus predicted <NAT>
F; 200-327/Domain: alpha-amylase ecre homology <AMY>
F; 200-327/Domain: alpha-amylase secore homology <AMY>
F; 200-327/Domain: alpha-amylase core homology <AMY>
F; 204/Painding site: calcium (Asn) (covalent) #status predicted
F; 148, 189, 202. 237/Binding site: calcium (Asn) (covalent) #status predicted
F; 148, 189, 202. 237/Binding site: calcium (Asn) (covalent) #status predicted
F; 234/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 234/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 235/Active site: Asp, Glu, Asp #status predicted

Query Match
Best Local S; milarity 61.5%; Pred. No. 0.079;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 105 AYHGYWMKNIYKI 117

Search completed: November 7, 2005, 18:58:45
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976cc3 aspergillus

90206 aspergillus

90206 aspergillus

90207 aspergillus

905th4 aspergillus

971v45 aspergillus

971v45 aspergillus

9151 dictyostell

9151 dictyostellus

92194 cryptococcu

9521 aspergillus

91326 aspergillus

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910117 lipomyces k

$6051 thermoactin

97451 neurospora

92157 saccharomyc

910427 schizosacch

92157 saccharomyc

92157 schizosacch

92157 schizosacch

92158 achizosacch

939789 schizosacch

939789 schizosacch
                                                            ); Search time 6.97683 Seconds (without alignments) 954.162 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                              1612378 seqs, 512079187 residues
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Q13296
AMY1 LIPKO
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Q76CT3
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                         vibrio vin
vibrio chol
bacillus sp
paenibacill
bacillus sp
bacillus sp
bacillus sp
bacillus ci
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bacillus ci
bacillus ci
                   vibrio vuln
           vibrio para
 bacillus ci
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SWART; SWO642; Aamy; 1.
Calcium-binding; Carbobytate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Multigene family; Signal.
                                                                                                                                                                                                                                                                 Bukaryota; Pungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
         087fr2
07mc10
08dc311
09kd8186
P09121
0683e3
P1083e3
P10921
P17692
P43379
P43379
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Last annotation update)
rsor (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-amylase A.
Nucleophile (By similarity).
Proton donor (By similarity)
By similarity.
Calcium 1 (By similarity).
                                                                                                                                                                                     498 AA
                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52755; CAA36966.1; --
FIR; A48305; A48305.
HSSP; P10529; 7TAA.
INCEPPC; IPR006589; Alp amyl cat sub.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006046; Glyco hydro_13.
                                                           CDG2 PAEMA
CDGT BAC11
CDGT BACS0
CDGT BACS8
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               O7MCLO
QBD5L1
Q9KL86
CDGT BACS3
Q6S3E3
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                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                Alpha-amylase A precursor
glucanohydrolase A).
Name=AMYA;
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2227
2251
318
142
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22
227
251
318
142
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25-0CT-2004
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Q02905;
 CHAIN
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SEQUENCE FROM N.A.
MEDLINE=90128276; Pubmed=2612911; DOI=10.1016/0378-1119(89)90506-4;
TBUKAGOSHI N., PUTUKAWA M., Nagaba H., Kirita N., Tsuboi A., Udaka S.;
"Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
evidence for multiple related genes.";
Gene 84:319-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Takahashi K., Hara S., Yoshizawa K.; Tada S., Iimura Y., Gomi K.; Tada S., Iimura Y., Gomi K.; "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6; Genes M.J., Dove M.J., Seligy V.L.; "Aspergilus oryzae has two nearly identical Taka-amylase genes, each containing eight introns."; Genes 79:107-117(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
Brzozowski A.m., Davies G.J.;
"Structure of the Aspergilus oryzae alpha-amylase complexed with the inhibitor acarbose at 2.0-A resolution.";
Biochamistry 35:10837-10845(1997).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 206-225. MbMed=4733850; MBDLINE=74001521; PubMed=4733850; IBemura S., Ikenaka T.; amylase T. mhe amino acid sequences of glycopeptides obtained from Taka-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-80227691; Pubmed-6156152;
Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
Toda H., Narita K., Kakudo M.;
"Molecular structure of taka-amylase A. I. Backbone chain folding at
                                               Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                         Wirsel S., Lachmund A., Wildhardt G., Ruttkowski E.; "Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
MEDLINE-84212370; PubMed=6609921;
Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
"Structure and possible catalytic residues of Taka-amylase A.";
J. Biochem. 95:697-702(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 22-499.
Toda H., Kondo K., Narita K.;
The complete amino acid sequence of Taka-amylase A.";
Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975)
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Agric. Biol. Chem. 53:593-599(1989)
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                                                                                                                                                                                   STRAIN=DSM 63303;
MEDLINE=89237897; PubMed=2785629;
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J. Biochem. 87:1555-1558(1980).
                                                                                                                                                                                                                                                                                                    Mol. Microbiol. 3:3-14(1989).
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                                                                                                                  NCBI_TaxID=5062;
                          Name=AMY3;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TAXID=40384;
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
By similarity.
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submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AB109452; BAD01051.1; -.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:alpha-amylase activity; IEA.
InterPro; IPR00647; Alpha_amylat.at.
InterPro; IPR00647; Alpha_amylat.at.
InterPro; IPR00646; Glyco.hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
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P10529; P11763; Q00250;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A)
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E 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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MEDLINE-90254827; PubMed=2340591;
Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
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1D AMYB ASPAW

AC 002006;

DT 01-0CT-1996 (Rel. 34, Created)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 25-0CT-2004 (Rel. 45, Last annotation update)

DE Alpha-amylase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                             -1-SUBUNIT: Monomer.
-1-BIOTECHNOLOGY: Used in the brewing industry to increase the fermentability of beer worts (including those made from unmalted cereals), in the starch industry to make high maltose and high DE syrups (starch saccharification), in the alcohol industry to reduce fermentation time, in the cereal food industry for flour supplementation and improvement of chilled and frozen dough, and in the forestry industry for low-temperature modification of starch. Sold under the name Fungamyl by Novozymes.
-1-MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
-1-SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
-1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations.
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R PDB; GTAA; X-ray; G=22-499.
R PDB; TAAA; X-ray; G=22-499.
R GlycoSuiteDB; P10529; A=22-499.
R InterPro; IPR006689; Alp_amyl_cat_sub.
InterPro; IPR006647; Alpha amyl_cat.
InterPro; IPR006647; Alpha amyl_cat.
InterPro; IPR006128; Alpha-amylase; I.
R PRINTS; PR00110; ALPHAAMYLASE.
R SWART; SM00642; Aamy; I.
W 3D-structure; Calcium-binding; Carbohydrate metabolism;
W birect protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
FILLIGENE family; Signal.
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Calcium 1 (via carbonyl oxygen).
Calcium 1.
Calcium 2.
Calcium 1 (via carbonyl oxygen).
Calcium 2.
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/FTId=CAR 000125.
Q -> R (in AMY3).
F -> L (in AMY3).
T -> DC (in Ref. 5).
Q -> T (in Ref. 5).
D -> Y (in Ref. 3).
P -> L (in Ref. 3).
G -> V (in Ref. 3).
D -> H (in Ref. 3).
L -> L (in Ref. 3).
L -> L (in Ref. 5).
L -> L (in Ref. 5).
L -> S (in Ref. 5).
VPIX -> PYI (in Ref. 5).
L -> S (in Ref. 5).
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-> S (in Ref. 5).
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EMBL; X12726; CAA31219.1; --
EMBL; X12727; CAA31220.1; --
EMBL; D00434; BAA00336.1; --
EMBL; M33218; AAA32708.1; --
PIR; JX0201; JX0201.
PIR; JY0466; JT0466.
PIR; S04548; ALAS1.
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                 MEDLINE=92223146; PubMed=1368777;

Shibuya I., Tamura G., Ishikawa T., Hara S.;

Shibuya I., Tamura G., Ishikawa T., Hara S.;

Cloning of the alpha-amylase conv. of Aspergillus shirousamii and its expression in Saccharomyces cerevisiae.";

Biosci. Biocchanol. Biochem. 56:174-179(1992).

-!- CATALYTIC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic.

-!- CATALYTIC Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).

-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006046; Glyco_hydro_13.
Pram; PR00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAWILASE.
SWART; SW00642; Aamy; 1.
Hydrolase; Signal.
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Aspergillus oryzae.
Bukaryota; Fungl; Ascomycota; Pezizomycotina; Eurotiomycetes;
Bukaryota; Fungl; Ascomaceae; mitosporic Trichocomaceae; Aspergillus.
BUSI_TaxID=5062;
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Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen)
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Calcium 1 (via carbonyl oxygen)
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                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.,
"Cloning, characterization, and expression of two alpha-amylase genes
from Aspergullus niger var. awamori.";

Curr. Genet. 17:203-212(1990).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P10529; 777A.

InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006046; Alpa_amyl_cat.
InterPro; IPR006046; Glyco hydro_13.

Pfam; PF00128; Alpha-amylase; 1.

PRINTS; PR00010; ALPHAAWYLASE.
SMART; SM00642; Aamy; 1.

Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-amylase B.

Nucleophile (By similarity).

Proton donor (By similarity).

By similarity.

Calcium 1 (By similarity).

Calcium 1 (via carbonyl oxygen) (By similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

Calcium 1 (via carbonyl oxygen) (By similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

By similarity.

By similarity.
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01-APR-1993 (Rel. 25, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.00017;
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Best Local Similarity 100.
Matches 13; Conservative
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318
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218
29 AA;
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P30292;
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ACT SITE
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SEQUENCE
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Gaps

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0; Indels

499 AA

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(By similarity)

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Takhoury A.M., Woloshuk C.P.;

Takhoury A.M., Takhoury C.M., A.M., A.M., A.M., DEPLATANALINARIA C.M., A.M., A.M., A.M., A.M., A.M., DEPLATANALINARIA C.M., DEPLATAN
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 78; DB 2; Length 499; 100.0%; Pred. No. 0.00017;
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                                                                                                                                                                                                             Q7LV45;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylase (EC 3.2.1.1).
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Best Local Similarity 100.0%;
Matches 13; Conservative (
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             99 AYHGYWQQDIYSL 111
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                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                 Name=amyl;
Aspergillus flavus.
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                                                                                                               RESULT 8
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                                                                                                                                                                                                                                                   1. Biosci. Biotechnol. Biochem., 64:816-827(2000).
2. I. SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
3. RaBLi, BAD(1876; BAA95703.1; -...
3. RABLi, BAD(1876; BAA95703.1; -...
3. ROIS 98; JN0588.
3. RISP; P10529; 7TAA.
40; GO:0004556; F:alpha-amylase activity; IEA.
40; GO:0004556; F:alpha-amylase activity, acting on glycosyl bonds; IEA.
3. ROIS 98; F:alpha-amylase activity, acting on glycosyl bonds; IEA.
3. ROIS 98; F:alpha-amylase activity, acting on glycosyl bonds; IEA.
3. ROIS 98; F:alpha-amylase activity, acting on glycosyl bonds; IEA.
3. RIAETPO: IRR006649; Alpha-amylase; 1.
3. RABLY: SM00642; Amy; 1.
3. RABLY: SM006442; Amy; 1.
3. RABLY: SM006444; Amy;
                                                                                                                                                            "Molecular cloning and characterization of a transcriptional activator gene, amyR, involved in the amylolytic gene expression in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Sukaryota: Pungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NGB_TaxID=105351;
                                  STRAIN=RIB40;
BDDLINE=20289310; PubMed=10830498;
Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
Iimura Y.;
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-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL, AB083159; BAD0602.1; -.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006049; Alp amyl_cat sub.
InterPro; IPR006046; Glyco_hydro_l3.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 78; DB 2; Length 499; 100.0%; Pred. No. 0.00017; live 0; Mismatches 0; Indels
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SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylase precursor.
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Best Local Similarity 100.(
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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SIGNAL
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Gaps

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0; Indels

A BOREN N.A., Murphy R.M., Kelly J.M.;

L. SUMMILARITY: Belonge to family 13 of glycosyl hydrolases.

A 1-- SIMILARITY: Belonge to family 13 of glycosyl hydrolases.

EMBL; AP208225; APF1703.1;

R GO; GO:0004255; F:alpha-amylase activity; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR00604; Alpha amyl cat sub.

InterPro; IPR006046; Glyco\_hydro\_13.

R InterPro; IPR006046; Glyco\_hydro\_13.

R InterPro; IPR006046; Glyco\_hydro\_13.

PEam; PP00128; Alpha-amylase; 1.

PRINTS; PR00110; ALPHAAMYLASE. Name=amyå; Emericella nidulans (Aspergillus nidulans). Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella. Last sequence update)
Last annotation update)

1 AYHGYWQQDIYSL 13

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115-JUL-1998 (Rel. 36, Lat sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
31-JUL-1998 (Rel. 45, Last annotation update)
32-OCT-2004 (Rel. 45, Last annotation update)
33-OCT-2004 (Rel. 45, Last annotation update)
34-SCHAZORORGES (Melotic expression up-regulated protein 30).
34-SCHAZORORGES (Melotic expression up-regulated protein 30).
35-DAGASACHARBES (Melotic expression up-regulated protein 30).
36-DAGASACHARBES (Melotic expression up-regulated protein 30).
36-DAGASACH
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83.3%; Pred. No. 0.0018;
ive 2; Mismatches 0; Indels
                                                                               Query Match
96.2%; Score 75; DB 2; Length 490;
Best Local Similarity 92.3%; Pred. No. 0.00053;
Matches 12; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loomis W.F., Iranfar N.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF020284; AAB70852.1; --
HSSP; P10529; 7TAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 AA; 14950 MW; 2ACE8FDC55E79637 CRC64;
     SMART; SM00642; Aamy; 1.
SEQUENCE 490 AA; 54249 MW; A891C4ACEAEB5305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBI_TaxID=44689;
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Last annotation update)
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DiccyBase; DDB0214924; amyA.
GO; GO:0005975; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
IEA-TPCP: PR006047; Alpha amyl cat.
PF00128; Alpha-amylase; 1.
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                                                                                                                                                                                                                                                    91 AYHGYWQQDIYAL 103
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Matches 10; Conservative
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NCBI_TaxID=4896;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Allower K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutter S., Saunders D., Saeger K., Sharp S., Rutherford K., Rutter S., Saunders D., Stevens K., Miller S., Stevens K., Miller S., Stevens K., Miller S., Willer S., Stevens R., Squares R., Squares S., Stevens T., Whitehead S., RA Taylor K., Taylor R., Taylor K., Taylor K., Roller S., Miller R., Roller J., Volckaert G., Aert R., Robben J., Grymonprez B., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., R. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Adelibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Adelibert R., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Adelibert R., Revlella J.L., Moreno S., Amaricong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Marian, A., Marian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pombe.",
Nucleic Acids Res. 29:2327-2337(2001).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00642; Aamy; 1. Calcium-binding, Carbohydrate metabolism; Glycoprotein; Glycosidase; Hydrolase; Meiosis; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=21270454; PubMed=11376151; DOI=10.1093/nar/29.11.2327; Matanabe T., Miyashita K., Saito T.T., Yoneki T., Kakihara Y., Nabeehima K., Kishi Y.A., Shimoda C., Nojima H.; "Comprehensive isolation of meiosis-specific genes identifies novel proteins and unusual non-coding transcripts in Schizosaccharomyces
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Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen)
similarity).
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Nucleophile (By similarity).
Proton donor (By similarity).
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Calcium 2 (By similarity)
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InterPro, IPR006047; Alpha amyl_cat.
InterPro, IPR006589; Alp amyl_cat_sub.
Pfam; PF00128; Alpha-amylase; 1.
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SEQUENCE FROM N.A.

STRAINE-96431320; PubMed=8836148;

MEDLINE-96431320; PubMed=8836148;

A lefuji H., Chino M., Kato M., Iimura Y.;

Raw-etarch-digesting and thermostable alpha-amylase from the yeast Cryptococcus sp. S-2: purification, characterization, cloning, and sequencing.;

T Raw-etarch-digesting and thermostable alpha-amylase from the yeast Cryptococcus sp. S-2: purification, characterization, cloning, and sequencing.;

Biochem. J. 318:889-996(1996).

EMBL; D83541; BAA12010.1; -..

RBBL; D83540; BAA12010.1; -..

RBRSP; P10529; TTAA.

RSP; P10529; TTAA.

RGO; G0:0003556; F:alpha-amylase activity; IEA.

GO; G0:000356; P:catalytic activity; IEA.

GO; G0:0005975; P:catalytic activity; IEA.
                                                                                                                                                                               Cryptococcus sp. S-2.
Bukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellomycetidae incertae sedis; Cryptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase)
Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotlales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5061;
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
488 By similarity.
162 N-linked (GlcNAc. . .) (Potential)
157 N-linked (GlcNAc. . .) (Potential)
58715 MW; 455DD97FA428C182 CRC64;
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                                       85.9%; Score 67; DB 1; Length 513; 76.9%; Pred. No. 0.012; Live 2; Mismatches 1; Indels
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Pred. No. 0.022;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                               alpha-amylase.
8196B7B6E1D707E5 CRC64;
                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylage precursor.
                                                                                                                              631 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 AA.
                                                                                                                                                                                                                                                                                                                                           GG; WCJUZ8; Alpha-amylase; 1.
Pfam; PF00128; Alpha-amylase; 1.
Probom; PD001568; GBM 20; 1.
Probom; PD001568; Glyco_hydro_CBD; 1.
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21 631 a.
631 AA; 67658 MW;
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Local Similarity 76.9%;
He 10; Conservative 1
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SMART; SM00642; Aamy; 1
454 4
162 1
357 3
513 AA;
                                               Similarity
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Q92394;
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Calcium 1 (via carbonyl oxygen)
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Calcium 1 (via carbonyl oxygen).
Calcium 2.
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                              Claros M.G., Abarca D., Fernandez-Lobato M., Jimenez A.;
"Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase from Schwanniomyces occidentalis.";
Curr. Genet. 24:75-83(1993).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                    linkages in oligosaccharides and polysaccharides.
-!- CORACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006647; Alpha_amyl_cat.
InterPro; IPR006046; Glyco hydro_13.

Pfam; PF00128; Alpha-amylase; I.

PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy, 1.

Hydrolase; Signal.
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Eukaryotal, Pungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=105351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-amylase 2.
Nucleophile (By similarity).
Proton donor (By similarity).
By similarity.
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
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55966 MW; 3A562E95BD8AAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity).
(By similarity).
(via carbonyl oxygen)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.037;
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STRAIN=ATCC 26077 / CBS 2863;
MEDLINE=93365041; PubMed=8358835;
                                                                                                                                                                                                                                                                                                                                               EMBL; X73497; CAA51912.1; -. PIR; S33921; S33921.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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nes 9; Conservative
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Saccharomycetales, Saccharomycetaceae, Debaryomyces
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29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase 2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase 2).
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Pred. No. 0.035;
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76.9%;
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                           AMY2_DEBOC
Q08806;
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RN [1]

RA SEQUENCE FROM N.A.

RC STRAIN=KT-11;

RA Mateubara T. 1;

RA SUDMILTER ABO83162; BAD06005.1; -.

DR EMBL; AB083162; BAD06003.1; -.

DR GO; GO:0005976; F:alpha-amylase activity; IEA.

DR GO; GO:0005976; F:alpha-amylase activity; IEA.

DR GO; GO:0005976; P:alpha-amylase activity; IEA.

DR InterPro; IPR006047; Alpha amyl cat sub.

DR InterPro; IPR006045; Alpha-amylase; 1.

DR PFOOM; PF006189; Alpha-amylase; 1.

DR PFOOM; PF0001568; Glyco_hydro_CBD; 1.

DR PFOOM; PF0001568; Glyco_hydro_CBD; 1.

DR SWART; SM00642; Aamy; 1.

RY Signal.

PT 31GNAL

SQ SEQUENCE 634 AA; 69242 MW; 16C0BE6AF6PB0E9B CRC64;

ACHIEVED SIGNAL

SQ SEQUENCE 634 AA; 69242 MW; 16C0BE6AF6PB0E9B CRC64;

AL AYHGYMODIYSE 13

MATCHES 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DD 99 AYHGYMODIXSE 13

DD 99 AYHGYMODIXSE 13
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Search completed: November 7, 2005, 18:52:30 Job time: 7.97683 secs



34, Appl 35, Appl 76, Appl 77, Appl 2, Appl 1, Appl 1, Appl 2, Appl 2, Appl 1, Appl 1,

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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US-08-469-202-27
US-08-469-202-28
US-08-484-434C-34
US-09-384-361-34
US-09-384-361-34
US-09-384-361-35
US-08-947-965-71
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US-08-816-105A-1
US-08-816-607-2
US-09-845-707B-2
US-09-845-707B-2
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Sequence 10, 7
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-459-610-7
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US-09-182-859-7
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US-09-182-859-7
US-09-636-252A-10
US-10-186-042-7
US-09-636-252A-10
US-08-30-715A-2
US-08-30-715A-2
US-08-477-656B-2
US-08-477-81-6
US-08-477-81-8
US-08-477-81-8
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US-08-477-965-72
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Gapop 10.0 , Gapext 0.5
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                                                                                        Run on:
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUNTRY: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,899
FILING APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: LOWING DF., KAREN A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054,214-US
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPRA: 212-867-0123
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
ALIGNMENTS
                                                                                                                                                                                           APPLICANT: Bisgaard-Frantzen, Henrik APPLICANT: Borchert, Torben Vedel APPLICANT: Svendsen, Allan APPLICANT: Svendsen, Marianne APPLICANT: Van der Zee, Pia TITLE OF INVENTION: AMYLASE VARIANTS UNMERS OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 57534600 NO. 5753460di
                                                                                                                     ; Sequence 7, Application US/08720899; Patent No. 5753460; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-720-899-7
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Best Local Similarity
Matches 13; Conserv
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Sequence

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US-08-600-908A-10

Sequence 10, Application US/0860090BA

Patent No. 5989169

GENERAL INFORMATION:

APPLICANT: Svendean, Allan

APPLICANT: Bisg rd-Frantzen, Henrik

APPLICANT: Bisg rd-Frantzen, Henrik

APPLICANT: Borchert, Torben Vedel

ITITLE OF INTENTION: 'Amylase Mutants

NUMBER OF SEQUENCES: 13

CORRESPONDENCE BISS:

ADDRESSEE: No. 59891690 No. 5989169th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STRIET: 405 Lexington Avenue, 64th Floor

CITY: New York

STRIET: 405 Lexington Avenue, 64th Floor

CONTYRY: United States of America

STRIET: 10174-6401

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER IBM PC compatible

OPERATING SYSTEM: PC compatible

OPERATING SYSTEM: PC compatible

OPERATING SYSTEM: DC 0908/MS-05

SOFTWARE: A35

ATTORNEY AGENT INFORMATION:

NAME: Green, Reza

RESTSCRACTION UNFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRORE 212-867-0123

TELEFRORE 212-867-0123

TELEFRORE 212-867-0123
SEE: No. 58308370 No. 5830837disk of No. 5830837th America, Inc.: 405 Lexington Avenue, 64th Floor
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 78; DB 2; Length 478; 100.0%; Pred. No. 0.00012;
                                                                                                                                       CUMTRY: USA

ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/343,804
FILING DATE: 22-NOV-1994
FILING DATE: 22-NOV-1994
FILING DATE: 22-NOV-1994
FILING DATE: LOWARTION:
NAME: LOWARTION: ASEN AREN A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
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100.0%; Score '8; ub
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 13; Conservative 0; Mismatches
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INFORMATION FOR SEQ ID NO:
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                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUDRESSE:
AUDRESSE:
AUDRESSE:
AUGUSTATE:
New York
STREET:
New York
STATE:
New York
COUNTRY:
COUNTRY:
USA
ZIP:
10174-6401
COMPUTER READABLE FORM:
MEDIUM TYEE:
COMPUTER:
DEBATIOS SYSTEM:
PC-DOS/MS-DOS
SOFTWARE:
PATELING BATE:
APPLICATION NUMBER:
FILING APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATTOMATION TO SAME AND APPLICATION NUMBER:
ATTOMATION TO SAME AND APPLICATION NUMBER:
ATTOMATION NUMBER:
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ATTOMATION NUMBER:
TELECOMMUNICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bisgaard-Frantzen, Henrik APPLICANT: Borchert, Torben Vedel APPLICANT: Svendsen, Allan APPLICANT: Thellersen, Marianne APPLICANT: Van der Zee, Pia TITLE OF INVENTION: AMYLASE VARIANTS NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58010430 No. 5801043di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendeen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                        Sequence 7, Application US/08459610 Patent No. 5801043 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08343804 Patent No. 5830837 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                              1 AYHGYWQQDIYSL 13
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Best Local Similarity 100.
Matches 13; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-459-610-7
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Gaps

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ch 100.0%; Score 78; DB 3; Length 478; 1 Similarity 100.0%; Pred. No. 0.00012; 13; Conservative 0; Mismatches 0: Indele
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                                                                                                                                                  TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT APPLICATION NUMBER: 0515/96
EARLIER APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
EARLIER APPLICATION NUMBER: 0712/96
EARLIER APPLICATION NUMBER: 0775/96
EARLIER APPLICATION NUMBER: 0775/96
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEC ID NOS: 37
LENGTH: 478
LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITLE REFENDE: 4796,204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-11-08
                                                                                  APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
       Sequence 7, Application US/09182859
Patent No. 6143708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 AYHGYWQQDIYSL 90
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 478
TYPE: PRT
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Sequence 10, Application US/08683838A

Setent No. 60227244

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bigs id-Franzen, Henrik
APPLICANT: Bigs id-Franzen, Henrik
APPLICANT: Bigs id-Franzen, Henrik
APPLICANT: Borchert, Torben Vedel
ITITLE OF INFURINION: 'Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
STREET: Now York
COUNTRY: United States of America
ZIP: Now York
CONFURTS: INW YORK
STATE: Now York
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP Compatible
OFFERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
FILING DATE:
CLASSIFICATION NUMBER: US/08/693,938A
FILING DATE: 11-FEB-1996
ATTORNEY/AGENT INFORMATION:
FILING DATE: 11-FEB-1996
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 212-867-0123
TELEPRONE CLASSIFICATION
TELEPHONE: 212-867-0123
TELEPRONE CLASSIFICATION
SEQUENCE CLARACTERISTICS:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CLARACTERISTICS:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CLARACTERISTICS:
INFORMATION CACHAGE
INFORMATION ACTION
TELEPHONE: 212-867-0123
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CLARACTERISTICS:
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                                                                                                                                                                                                       Query Match 100.0%; Score 78; DB 2; Length 478; Best Local Similarity 100.0%; Pred. No. 0.00012; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 78; DB 3; Length 478; 100.0%; Pred. No. 0.00012;
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                       LENGTH: 478 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-600-908A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 478 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                          78 AYHGYWQQDIYSL 90
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Best Local Similarity 100.
Matches 13; Conservative
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SEQUENCE CHARACTERISTICS
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US-08-683-838A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-683-838A-10
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US-09-182-859-7
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US-08-339-715A-2
; Sequence 2, Application US/08339715A
; Patent No. 5965442
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                                                                                           APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Trantzen, Henrik
APPLICANT: Bisgard-Trantzen, Henrik
APPLICANT: Bisgard-Trantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
FRIOR APPLICATION NUMBER: 09/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PSESEQ for Windows Version 3.0
SSOFTWARE: PSESEQ for Windows Version 3.0
LENGTH: 478
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COSTILLED POSTORY

CONTROLL DIVENATION

CONTROLL INFORMATION

APPLICANT: Svendsen, Allan

APPLICANT: Svendsen, Allan

APPLICANT: BISGRACT FRANTZEN, HENRIK

TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 4796.204-US

CURRENT FILING DATE: 2002-06-28

FRIOR PELICATION NUMBER: US/09/672,459

PRIOR PELICATION NUMBER: 09/182,859

PRIOR FILING DATE: 1998-10-29

PRIOR PILING DATE: 1996-06-28

PRIOR PILING DATE: 1996-07-11

PRIOR PILING DATE: 1996-07-11

PRIOR FILING DATE: 1996-07-11

PRIOR FILING DATE: 1996-07-11

PRIOR FILING DATE: 1996-11-08

NUMBER OF EKQ ID NOS: 37

SOFTWARR: FABELEKQ for Windows Version 3.0

SEQ ID NO 7
                                                  Sequence 10, Application US/09636252A
Patent No. 6440716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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Best Local Similarity 100.
Matches 13; Conservative
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  RESULT 8
US-09-636-252A-10
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78 AYHGYWQQDIYSL 90

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Variant Gene Of The Enzyme And Method For Producing
Oligosaccharide Using The Enzyme
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GENERAL INFORMATION:
APPLICANT: Kaneko, Hiroki
APPLICANT: Takada, Usobikazu
APPLICANT: Shimada, Jiro
APPLICANT: Shimada, Jiro
APPLICANT: Yanase, Michiyo
APPLICANT: Yanase, Michiyo
APPLICANT: Takata, Hiroki
APPLICANT: Okada, Shigetaka
TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
TITLE OF INVENTION: NEOPULLULANASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62; DB 2; Length 478;
Pred. No. 0.044;
                                                                                                                                                                                                                                                                       ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
STREET: Metropolitan Square Building, Suite 800, 1450
STREET: G. Street
CITY: Washington
STATE: D.C.
COUNTRY: USA
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MEDITOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,715A
FILING DATE: 14-NOV-1994
CLASSIFICATION NUMBER: JD 306096/1993
ATTORNEY/AGENT INFORMATION:
NAME: Melser, Allen S.
REGISTRATION NUMBER: 18335.009
TELECOMMUNICATION INFORMATION:
TELEPRAK: 202-824-8199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kazuhiko; APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant Gene Of
TITLE OF INVENTION: Oligosaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LELEX: 248516
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENGTH: 478 ami-
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TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 84.6
Matches 11; Conservative
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US-08-339-715A-2
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US-08-467.331-6
US-08-467.331-6
US-08-467.331-6
US-08-467.331-8
US-08-467.331-
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                                                                     NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-
TELEPHONE: (703) 205-8000
TELEX: (703) 205-8050
TELEX: 243345
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acids
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
    FILING DATE: 02-MAR-1994 ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 53.8
Matches 7; Conservative
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79 AYHGFWMKNIYKI 91
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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US-08-470-702-6
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Sequence 6, Application US/08470702

Patent No. 5631149

GENERAL INFORMATION:

HOPLICANT: MATSUI, IKUO

APPLICANT: MATSUI, IKUO

APPLICANT: MYAIRI, SACHIO

TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,

TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,

TITLE OF INVENTION: VARIANT GENE OF THE ENZYME

TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME

NUMBER OF SEQUENCES:

ADDRESSEE: BILO GATCHOUSE Road, Sulte 500 East

CONNESPONDENCE ADDRESS:

STATE: VITGINIA

STATE: VITGINIA

COUNTY: Falls Church

STATE: VITGINIA

COUNTY: U.S.A.
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                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

SURRENT APPLICATION NUMBER: US/08/204,656B

FILING DATE: 02-MAR-1994

CLASSIFICATION: 435

ATORNEY/AGENT INFORMATION:

NAME: Weiner: Marc S.

REGISTRATION NUMBER: 234-252P

TELEROMENINCATION INFORMATION:

TELEROMENICATION INFORMATION INFORMATION:

TELEROMENICATION INFORMATION I
                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 53.8-
Best Local Similarity 53.8-
Conservative
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79 AYHGFWMKNIYKI 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
NUMBER OF SEQUENCES: 1
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US-088-204-656B4-4
US-088-204-656B4-4
Sequence 4, Application US/08204656B
Patent No. 553882
Patent No. 523882
Patent Niyairi, Sachio
Papticanr: Honda, Koichi
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: ADDRESS:
ADDRESSER: Blich, Stewart, Kolasch & Birch, LLP
STREET: Virginia
COUNTRY: U.S.A.
STREET: Virginia
COMPUTER: INP PC compatible
COMPUTER: INP PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/204,656B
FILING DATE: Weiner, Marc S.
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32.181
REFERENCE/DOCKET NUMBER: 32.181
REFERENCE/DOCKET NUMBER: 32.181
REFERENCE/DOCKET NUMBER: 32.181
REFERENCE (703) 205-8050
TELEFONE: (703) 205-8050
TELEFONE: TELECOMMUNICATION INFORMATION:
TELEFONE: TELEFONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                        Score 54; DB 1; Length 468; Pred. No. 0.82;
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US-08-470-702-7
; Sequence 7, Application US/08470702
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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79 AYHGWWMKNIYKI 91
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MOLECULE TYPE: protein
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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HYPOTHETICAL: 
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COUNTRY: U.S.A.

ZIP: 22042

ZIP: 22042

COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION NAMBER: US/08/470,702
FILING DATE: 102-MAR-1994
ATTORNEY/AGENT INPORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/POCKET NUMBER: 33,181
REFERENCE/POCKET NUMBER: 234-252P
TELECOMMUNICATION INPORMATION:
TELEBOONE: (703) 2.05-8000
GENERAL INFORMATION:

APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HY
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HY
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME A:
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE EN
NUMBER OF SEQUENCES: 17
CORRESPONDESSE: 17
CORRESPONDESSE: ADDRESSE: AD
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Pred. No. 1.2;
4; Mismatches
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 53.8%;
Matches 7; Conservative
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40, Appl 45, Appl 42, Appl 1246, Appl 1246, Appl 1246, Appl 1, Appl 1,

Sequence

Sequence Sequence Sequence Sequence Sequence

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

Sequence 1 Sequence 2 Sequence 3

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence 45, Sequence 42, Sequence 13, Sequence 124 Sequence 222 Sequence 48,

Sequence

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Length 476;
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Sublication No. US20050054071A1

GENERAL INFORMATION:

APPLICANT: Talar, Rikako

APPLICANT: Talain, Eric

APPLICANT: Allain, Eric

APPLICANT: Hort, Carsten

APPLICANT: Uikso-Nielsen, Anders

TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING

TITLE OF INVENTION: HYBRID ENZYMES

CURRENT APPLICATION NUMBER: US/10/877,849

CURRENT FILING DATE: 2004-06-25

NUMBER OF SEQ ID NOS: 43

SEQ ID NOS: 43
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US-10-797-393A-5
US-10-877-849-40
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US-10-228-063-45
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US-10-213-990-42
US-10-213-990-42
US-10-213-990-48
US-10-369-493-12469
US-10-13-990-48
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US-10-877-849-34
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US-10-486-18-32
US-10-486-18-32
US-10-369-493-22
US-11-021-951-44
US-10-385-305-108
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llarity 100.0%; Pred. No. 0.0011;
Conservative 0; Mismatches 0;
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     TYPE: PRT
ORGANISM: Aspergillus oryzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43
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Best Local Similarity
Matches 13; Conserv
   US-10-877-849-43
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                                                                                                                                                (without alignments) 771.303 Million cell updates/sec
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                                                                                                                              2005, 18:11:05 ; Search time 7.05212 Seconds
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-186-042-7
US-10-644-187-7
US-10-926-720-10
US-10-980-759-7
US-11-064-196-10
US-10-815-495-22
US-10-815-495-30
US-10-815-495-30
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Maximum Match 100%
Listing first 45 summaries
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                                                                                            - protein search, using sw model
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seq length: 200000000
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Gaps

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Score

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LENGTH: 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/10186042;
Publication No. US20030171236A1
GENERAL INFORMATION:
APPLICANT: Svendeen, Allan
APPLICANT: Blegard-Frantzen, Henrik
APLICANT: Blegard-Frantzen, Henrik
TILE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT PILING DATE: 2002-06-28
PRIOR PILING DATE: 12000-09-28
PRIOR PILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1996-07-11
PRIOR FILING DATE: 1996-07-30
PRIOR FILING DATE: 1996-07-30
PRIOR FILING DATE: 1996-07-11
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                                      Sequence 10, Application US/10184771
Publication No. US2003017076941
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants;
CURRENT APPLICATION NUMBER: US/09/636,252
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR PILING DATE: 2000-08-10
PRIOR PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SSEQ ID NO 10
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; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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US-10-184-771-10
RESULT 2
US-10-184-771-10
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Matches
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GENERAL INFORMATION:

APPLICANT: Novozywes Biotech, Inc.

APPLICANT: Connelly, Mariah

APPLICANT: Brody, Howard

APPLICANT: Brody, Methods For Producing Biological Substances In Enzyme-Deficient

TITLE OF INVENTION: Mutants Of Aspergillus Niger

TITLE OF INVENTION: Mutants Of Aspergillus Niger

TITLE OF INVENTION WINDER: US/10/815,495

CURRENT APPLICATION NUMBER: US/10/815,495

CURRENT FILING DATE: 2004-03-31

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.2

SEQ ID NO 22

LENGTH: 498
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; Publication No. US20040229764A1
; GENERAL INFORMATION:
; APPLICANT: Blagard-Frantzen, Henrik
APPLICANT: Pedersen, Sven
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; TILE REFERENCE: 5835.200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
CURRENT FILING DATE: 2004-07
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR PILING DATE: 1999-11-16
; WUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Version 3.2
; SEQ ID NO 2
  FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION UNDRER: US/11/064,196
CURRENT FILING DATE: 2005-02-22
PRIOR PLING DATE: 2000-08-10
PRIOR FLING DATE: 2000-08-10
PRIOR FLING DATE: 1996-07-18
PRIOR FILING DATE: 1996-07-18
NUMBER: OF SEQ ID NOS: 16
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-815-495-22; Application US/10815495; Publication No. US20040191864A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Aspergillus niger
US-10-815-495-22
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Best Local Similarity 100.
Matches 13; Conservative
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Matches 13; Conservative
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; ORGANISM: A. Oryzae
US-11-064-196-10
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100.0%; Score 78; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels
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REFERENCE/DOCKET NUMBER: 4394.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFOGRATION:
APPLICANT: Svendeen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Busgard-Frantzen, Henrik
FILE REFERENCE: 4796.204-08
CURRENT APPLICATION NUMBER: US/10/980,759
CURRENT APPLICATION NUMBER: US/09/672,459
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 1090-09-28
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-11
PRIOR FILING DATE: 1996-06-11
PRIOR FILING DATE: 1996-06-11
PRIOR FILING DATE: 1996-06-11
PRIOR FILING DATE: 1996-01-11
PRIOR FILING DATE: 1996-01-11
PRIOR FILING DATE: 1996-01-108
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 7
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                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
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APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
                 TELECOMMUNICATION INFORMATION:
TELEPHN: 212-867-0123
TELEFAR: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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Publication No. US20050118695A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bacillus licheniformis US-10-980-759-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AYHGYWQQDIYSL 13
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Best Local Similarity 100.
Matches 13; Conservative
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; Sequence 40, Application US/10877849
; Publication No. USO050054071A1
; GENERAL INFORMATION:
    APPLICANT: Udagawa, Hiroaki
    APPLICANT: Tragi, Shinobu
    APPLICANT: Tragi, Shinobu
    APPLICANT: Allain, Eric
    APPLICANT: Hjort, Carsten
    APPLICANT: Vikso-Nielsen, Anders
    TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
    TITLE OF INVENTION: HYBRID ENZYMES
    CURRENT APPLICATION NUMBER: US/10/877,849
    CURRENT PILING DATE: 2004-06-25
    NUMBER: PatentIn version 3.2
    SOOTWARE: PatentIn version 3.2
    LENGTH: 608
    LENGTH: 608
                                                                                                        Sequence 5, Application US/10797393A

Publication No. US20040219649A1

GENERAL INFORMATION:

APPLICANT: Olsen, Hans Sejr

APPLICANT: Federsen, Sven

TITLE OF INVENTION:

FILE SEFERENCE: 10391.200-US

CURRENT APPLICATION NUMBER: US/10/797,393A

CURRENT APPLICATION NUMBER: 2004-03-10

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Artificial US-10-877-849-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Aspergillus oryzae
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99 AYHGYWQQDIYSL 111
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APPLICANT: Taira, Rikako
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Best Local Similarity
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LENGTH: 499
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Sequence 18, Application US/10815495
Publication No. US20040191864A1
GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Brody, Howard
APPLICANT: Brody, Howard
APPLICANT: Brody, Howard
ITILE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Mutants Of Aspergillus Niger
FILE REFERENCE: 10345.200-US
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 499
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Best Local Similarity 100.0%; Score 78; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 78; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                       Query Match
100.0%; Score 78; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30. Application US/10877849

Publication No. US200S0054071A1

GENERAL INPORMATION:
APPLICANT: Udagawa, Hiroaki
APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Allain, Eric
APPLICANT: Hjort, Carsten
CURRENT Hjort, Carsten
TITLE OF INVENTION: HYBID BNZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490.500-US
CURRENT APPLICATION NUMBER: US/10/877,849

CURRENT FILING DATE: 2004-06-25

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Aspergillus oryzae US-10-877-849-30
  ; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2
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US-10-815-495-18
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LENGTH: 498
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Matches 13; Conservative 0; Mismatches 0; Indels 0
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APPLICANT: Tkagi, Shinobu
APPLICANT: Allain, Eric
APPLICANT: Hjort, Carsten
APPLICANT: Hjort, Carsten
APPLICANT: Vikeo-Nielsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILLE REPRENENCE: 10490.500-US
CURRENT APPLICATION WUMBER: US/10/877,849
CURRENT FILLING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOPTWARE: Patentin version 3.2
SEQ ID NO 36
LENGTH: 640
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; ORGANISM: Aspergillus shirousami
US-10-228-063-45
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ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Artificial
US-10-877-849-36
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Search completed: November 7, 2005, 18:45:03 Job time : 8.05212 secs

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The sequence os that of the Asoergillus oryzae alpha amylase, sold commercially as FUNGAMY. (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amylase exhibits a better activity level and better stability in the presence of oxidising agents than previous mutant alpha amylases, and improved thermostability at moderately low pH. The enzyme can be used as an additive for detergents, dishwashing agents and liquifaction agents. (Updated on 25-MAR-2003 to correct PN field.)
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Copyright (c) 1993 - 2005 Compugen Ltd
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	andard; protein; 4  (revised) (first entry) a-amylase. substitution; stab agents; liquifact oryzae.  1.  92DK-0000946; 92DK-0000230.; 93DK-0000292: 0-NORDISK AS. Bisgard-Frantzen	∙d•d Ou
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Recombina

Aap70571 / Ads23436 | Aap81161 | Aap81180

Alpha-amy Bacteria]

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Oxidation stable alpha amylases can be used for the simultaneous desizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methiconine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or Asp. The parent alpha amylase is pref. derived from a Bacillus species, although alpha amylases of fungal origin can also be used. This sequence is the wild type (unmodified) alpha amylase of Aspergillus oryzae
                                                                                                                                         Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch; thermostable; methionine; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of an oxidation stable alpha-amylase - for simultaneous desizing and bleaching or scouring of fabrics contg. starch or starch derivs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl; Aspergillus oryzae; Bacillus amyloliquefaciens; altered property; calcium dependency; substrate binding; stability; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction; sweetener; ethanol production; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 13; DB 2; Length 478; 100.0%; Pred. No. 2e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae alpha-amylase (mature protein).
                                                                                                  Aspergillus oryzae alpha amylase (mature protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pedersen HH, Nilsson TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 25-26; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW14500 standard; protein; 478 AA.
                                                                                                                                                                                                                                                                                                                                                                                             94DK-00000141
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 AYHGYWQQDIYSL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marcher D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-283767/37.
                                                                                                                                                                                                 Aspergillus oryzae
                                                                                                                                                                                                                                      Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                             02-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                       05-OCT-1994;
                                                                                                                                                                                                                                                                            WO9521247-A1
                                                            17-JAN-1996
                                                                                                                                                                                                                                                                                                                   10-AUG-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUN-1997
                      AAR78270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toft AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, blacching and dyeing. The variants have improved thermostability, acid/alkaline stability; low temperature optimum; higher hydrolysis velocity and improved tolerance to other composition constituents, e.g. oxidation agents. (Updated on 25-MAR-2003 to correct PN field.)
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Bacillus derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance.
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                                      Score 13; DB 2; Length 478; Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 13; DB 2; Length 478; 100.0%; Pred. No. 2e-06;
                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus oryzae alpha amylase (mature protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bisgard-Frantzen H, Svendsen A,
                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 75-76; 105pp; English.
                                                                                                                                                                                                                                                      AAR72450 standard; protein; 478 AA.
                                    Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93DK-00001133.
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                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                   1 AYHGYWQQDIYSL 13
                                                                                                                                         78 AYHGYWQQDIYSL 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 AYHGYWQQDIYSL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVO-NORDISK AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus oryzae.
Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Der Zee P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borchert TV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-1994;
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02-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9510603-A1
                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
01-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-1995
                                                                                                                                                                                                                                                                                            AAR72450;
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Gaps

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Aspergillus oryzae.

AAR78270 standard; protein; 478 AA.

RESULT 3 AAR78270 ID AAR7

Matches

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/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 325-345 of AAM14498 is
deleted or replaced with a fragment corresponding to this
residue of a parent alpha-amylase (used as a template for a variant) corresponding to 196-198 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                               corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the mature Aspergillus oryzae alpha-amylase (A). Variants of parent termamyl- and fundamyl-like alpha-amylases (and methods of constructing them) are claimed. Examples of variants are featured above. The variants have altered properties such as calcium dependency, substrate binding and stability. Also one or more proline or cystein residues in the variant is modified or replaced with a non-proline or non-cystein residue such as alanine. The variants can be used for (dish)washing, as detergent additives or for fabric desizing or starch liquefaction. They can also be used for the production of
                                                                                                               Increasing amino acid fragment corresponding to this region is deleted from the parent sequence of a variant Fungamyl; claim 43".

291. 313

'label= loop 8 modification region

'note= at least one amino acid residue of a parent alphamylase (used as a template for a variant) correspondint to 322-346 of AAW14498 is deleted or replaced with a

    have altered
binding and stability.

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                                                                                                                                                                                                                                                                                                            fragment corresponding to this fragment; claim 36 297. .313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sweeteners and ethanol from starch. See also AAW14498-99
                                                                                                                                                                                                                                                                                                                                                             'label= loop 8 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-amylase variants and methods of production properties such as calcium dependency, substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borchert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 87-88; 171pp; English
                                                                  fragment; claim 23"
181. .184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragment; claim 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498
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95DK-00001192.
95DK-00001256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-DK000057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-371424/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
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                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-1995;
23-OCT-1995;
10-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9623874-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-1996
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Matches
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    요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residue of a parent alpha-amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-199 of AAW14499; claim 42"

165. 177

/label= loop 3 modification region

//note= "at least one amino acid residue of a parent alpha -amylase (used as a template for a variant) corresponding to 195-202 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102. 206

(Jabel= loop 3 modification region
/label= loop 3 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 121-181 of AAW14499 is
deleted or replaced with a fragment corresponding to this
fragment; claim 26"
                      13. .45
/label= loop 1 modification region
/label= loop 1 modification region
/label art least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 7-23 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 33"
                                                                                                                                                                                                                                                                                                                                                        /label= loop 1 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 12-19 of AAW14499 is deleted or replaced with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= loop 2 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as template for a variant) corresponding
to 44-57 of AAM14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as template for a variant) corresponding
to 117-185 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12. .38
/label= loop 1 modification region
/label= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 14-15 of AAW14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "at least one amino acid residue of a parent alpha -amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-206 of AAW14499; claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deleted
                                                                                                                                                                                                             /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 8-18 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template fa variant) corresponding to 48-51 of AAW14499 is delete or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "preferred region where at least one amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         fragment corresponding to this fragment; claim 30"
                                                                                                                                                                                          /label= loop 1 modification region
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                                                                                                                                                                                                                                                                                                              fragment; claim 35"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment; claim 20"
                                                                                                                                                                                                                                                                                                                                          28. .42
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    Key
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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The present invention relates to a method of producing heterologous hological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance and second nucleotide heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase A (amyA) protein.
                                                                                                                                                                                                                                    Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 13; DB 8; Length 498; 100.0%; Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus niger neutral alpha-amylase B (amyB) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                            Example 11; SEQ ID NO 22; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADT89628 standard; protein; 499 AA.
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                                                                                      (NOVO ) NOVOZYMES BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVOZYMES BIOTECH INC.
    31-MAR-2004; 2004US-00815495.
                                              31-MAR-2003; 2003US-0459902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2004; 2004US-00815495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2003; 2003US-0459902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYHGYWQQDIYSL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AYHGYWQQDIYSL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                Connelly M, Brody H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Connelly M, Brody H;
                                                                                                                                                                      WPI; 2004-708545/69.
N-PSDB; ADT89631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-708545/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2004191864-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADT89627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-2004.
                                                                                                                                                                                                                                                                                                       substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADT89628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
ADT89628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a fungamyl-like alpha-amylase. The specification describes variants of this fungamyl-like alpha-amylase, which have an alteration in one the amino acid regions 98-110, 150-160, 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or substitution of an amino acid or an insertion of an amino acid downstream of a particular position. The variants retain alpha-amylase activity, and have better heat stability and/or stability at acidic pH, relative to wild-type enzyme. The variants can therefore be used at higher temperatures (more efficient conversion or faster reaction, and have reduced need for cooling and reduced risk of contamination). The variants may also be used in conjunction with other enzymes, particularly of high maltose content, or alcohol, from starch, as dough improver for baked goods; in brewing, to increase fermentability of the wort, and for liquefaction of starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variant of Fungamyl-like alpha-amylase, useful for production of maltose syrups, includes mutations that improve stability against heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                          Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose; alcohol; starch; dough improver; brewing; starch liquification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13; DB 4; Length 49
Pred. No. 2.1e-06;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus niger neutral alpha-amylase A (amyA) protein.
Amino acid sequence of a fungamyl-like alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glucoamylase; glaA; amyA; alpha-amylase A; enzyme
                                                                                                                                                                                                                                                                                                                                                                   Pedersen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADT89632 standard; protein; 498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 42-45; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                   Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Sc
| Similarity 100.0%; P1
| 13; Conservative 0;
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                                                                                                                                                                                                                                                                              99DK-00001617
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                                                                                                                                                                                                                                                                                                                  (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-367478/38.
N-PSDB; AAF90208.
                                                                                                                                                                                                                                                                                                                                                                   Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                      Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 498 AA;
                                                                                                                                                WO200134784-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and acidic pH.
                                                                                                                                                                                                                                                                              10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-2004
                                                                                                                                                                                          17-MAY-2001
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Example 10; SEQ ID NO 18; 58pp; English

substance

US2004191864-A1.

98

Best Loca Matches

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30-SEP-2004

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Gaps

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The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide sequences comprising modification of glucoamylase (glah) and recovering heterologous biological substance.
                                                                                                                                                                                                                             Aspergillus niger neutral alpha-amylase B (amyB) protein.
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AYHGYWQQDIYSL 111 1 AYHGYWQQDIYSL 13 δ 셤

RESULT 8 ABP96630

ABP96630 standard; protein; 1095 AA. (first entry) 02-JUN-2003 ABP96630;

Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch; maltodextrin; ethanol; fermentation; beverage; enzyme. Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45. 

Aspergillus shirousami

Synthetic.

WO2003018766-A2.

06-MAR-2003

27-AUG-2002; 2002WO-US027129.

27-AUG-2001; 2001US-0315281P.

(SYGN ) SYNGENTA PARTICIPATIONS AG.

Batie CJ, Chen W, Craig J, Kinkema M; Lanahan MB, Basu SS,

WPI; 2003-268420/26. N-PSDB; ACC44572.

Novel polynucleotide encoding hyperthermophilic processing enzymes e.g. alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.

Claim 1; Page 107; 158pp; English

The present invention describes polynucleotides which encode processing enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose enzymes, or glucoamylase) that are optimised for expression in plants. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic processing enzymes, which are activated under suitable conditions to act upon the desired substrate. Also described are self-processing transgenic plants and plant parts, e.g. grain, which express one or more of these enzymes and have an altered composition that facilitates plant and grain processing. Also described is a method (M) for converting starch to starch-derived products in a transformed plant part (TPP), by activating the starch processing enzyme contained in it. Transgenic grain is useful for preparing maltodaxtrin. A transformed plant (TP) can be used to produce food products having improved taste and to produce fermentable

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         to mill or physically disrupt the integrity of plant parts prior to recovery of starch-derived products. The present sequence represents alpha-amylase/glucoamylase fusion protein, which is given in the exemplification of the present invention
                                                                                                                                                   Gaps
 (M) eliminates the
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                                                                                                                   Score 13; DB 6; Length 1095;
Pred. No. 3.8e-06;
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 substrates for ethanol and fermented beverages.
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0
                                                                                                                   100.0%;
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                                                                                                                                                     13; Conservative
                                                                                                                                                                                                          78 AYHGYWQQDIYSL
                                                                                                                     Query Match
Best Local Similarity
                                                                                       Sequence 1095 AA;
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Gaps

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Indels

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0; Mismatches

13; Conservative

Query Match Best Local Similarity Matches 13; Conserv

Sequence 499 AA;

100.0%; Score 13; DB 8; Length 499; 100.0%; Pred. No. 2.1e-06;

RESULT 9 ABB8017

ABB80177 standard; protein; 495 AA.

ABB80177;

(first entry) 11-AUG-2003

A. fumigatus AfAAL1.

beta-galactosidase, invertase, lipase, alpha-amylase, laccase, polygalacturonase, xylanase, gallate ester linkage, detergent, cellulose, glucase, oxygen, myo-inositol phosphate, lactose, tea leaf, sucrose, glyceride, starch, maltodextrin, oxidated phenolic compound, polygalacturonic acid chain, xylan, xylo-oligomer, food, feed, beverage, tannase; cellulase; glucose oxidase; glucoamylase; phytase;

Aspergillus fumigatus.

textile; tea liquor; cleaning ability

WO2003012071-A2.

13-FEB-2003. 

05-AUG-2002; 2002WO-US024842

03-AUG-2001; 2001US-0309870P

(ELIT-) ELITRA PHARM INC.

Roemer T, B, Storms R, Jiang

Bussey H;

WPI; 2003-332729/31

N-PSDB; ABQ80345, ABQ80346.

Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, Novel isolated Aspergillus fumigatus beverages, textiles and detergents.

Claim 17; Page 134-35; 169pp; English.

The sequences given in ABB80164-87 show enzymatic proteins derived from A. fumigatus. These proteins display the catalytic activity of an enzyme such as tannase, callulase, glucose oxidase, glucoamylase, phytase, betaglactosidases, invertase, lipase, alpha-amylase, laccase, polygalacturonase or xylanase. Compositions comprising the tannase are useful for modulating the amount of composition comprising the tannase are useful for modulating the amount of cellulose in a composition. Compositions comprising the amount of cellulose in a composition comprising phytase are useful for modulating the amount of myo-inositol phosphates in a composition. Composition comprising phytase are useful for modulating the amount of myo-inositol phosphates in a composition. Composition comprising comprising the amount of myo-inositol phosphates in a composition. Composition comprising comprising the amount of sucrose or invertase are useful for modulating the amount of sucrose in a composition. Compositions comprising sucrass or invertase are useful for modulating the amount of sucrose in a composition. Compositions comprising sucrass or invertase are useful for modulating the amount of sucrose in a composition comprising the amount of sucrose in a composition.

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                                                                                                                                                             for attachment to a nucleic acid array for examination of expression patterns, and to raise anti-protein antibodies. The polypeptide having tannase activity increases the yield of tea liquor from tea leaves, improves the colour, flavour and health benefits of tea products, particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermus sp. IM6501, maltogenic amylase; EC 3.2.1.133; crystallisation; protein co-ordinate data; 3 dimensional structure.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.
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                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                   92.3%; Score 12; DB 100.0%; Pred. No. 2.6 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus oryzae TAKA protein (TAA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 188; 196pp; Korean.
                                                                                                                                                                                                                                                                                                                                                         ABB09072 standard; protein; 423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99KR-00039130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POST-) POSTECH FOUND.
(SAMY-) SAMYANG GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                    97 AYHGYWQQDIYS 108
                                                                                                                                                                                                                                                                      12; Conservative
                                                                                                                                                                                                                                                                                         1 AYHGYWQQDIYS 12
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                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park GH;
                                                                                                                                                                                                                                 Sequence 495 AA;
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                                                                                                                                                                                                                                                                       Matches
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The present invention describes manufacturing maltogenic amylase (EC 3.2.1.133) having improved transglycosylation activity, comprising using crystallisation and the three dimensional structure of maltogenic

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camylase. Manufacturing maltogenic amylase comprises the following steps:

(1) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC 5027BP) and inserting the gene into plasmid pUCL19 to construct recombinant DNA (pThMA119); (ii) inserting the recombinant DNA to construct crecombinant DNA (pThMA119); (iii) inserting the recombinant DNA to crecombinant DNA (pThMA119); (iii) inserting the recombinant DNA to construct or contain a microbial cell; (iii) suspending the microbial cell with buffer solution at pH 7.5 and obtaining supernateant; and (iv) passing the supernateant through column chromatography and obtaining purified camplase. The maltogenic amylase is a dimer comprised of two caltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase (ThMA) crystal. The amylase has a structure containing an activated region that consists of amino acid residues of Asp. 128, (Iu-357, Asp. 424, and a pocket with glucose bound that consists of amino acid residues of cand a pocket with glucose bound that consists of amino acid residues of Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Ash1331, (Iu1332, Val1329, and Hisl360. The present sequence represents Aspergillus oryzae TAKA.

Cyctein (TAA), given in comparison with ThMA in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide from a filamentous fungus, preferably Aspergillus
niger, useful in a baking process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-amylase; enzyme; endohydrolysis; 1,4-alpha-glucosidic linkage; oligosaccharide; polysaccharide; baking.
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                                                                                                                                                                                                                                                                                                                                                                                      84.6%; Score 11; DB 4; Length 423; 100.0%; Pred. No. 0.00029;
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                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP97894 standard; protein; 494 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001EP-0000379.
2001EP-0000380.
2001EP-0000381.
2001EP-0000382.
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                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                 Sequence 423 AA;
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16-AUG-2001;
16-AUG-2001;
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16-AUG-2001;
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(first entry)

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Aspergillus niger acid alpha-amylase for ethanol production method
                                                           ADS75939 standard; protein; 484 AA.
78 AYHGYWQQ
                                                                                                             16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                     Olsen HS,
                                                                                      ADS75939;
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                                                                                      요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for producing ethanol from starch-containing material, by fermentation. The method involves carrying out a secondary liquefaction step in the presence of a thermostrable acid alphamylase. The method is used in producing ethanol from a starch-containing material such as tubers, roots or whole grain (e.g. corn, wheat or barley or their combination) or combination of the materials. Preferably ethanol is produced from starch-containing meterial that is obtained from cereals or from corns, cobs, wheat, barley, rye, milo and potatoes or their combination. The ethanol produced by above mentioned method is used as fuel alcohol and/or fuel additive. The ethanol is also useful as drinking ethanol i.e., potable neutral spirits or industrial ethanol. The present sequence is Aspergillus niger alpha-amylase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing ethanol from starch-containing material e.g., tubers, roots, whole grain, for use in fuel, by fermentation comprises carrying out a secondary liquefaction step in the presence of a thermostable acid alpha-
                                                                                                                                                                                                                                                                               starch; fermentation; liquefaction; alpha-amylase; additive; neutral spirit; industrial ethanol; enzyme.
                                                            Gaps
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100.0%; Pred. No. 0.64;
ive 0; Mismatches 0; Indels
                                  69.2%; Score 9; DB 6; Length 494;
100.0%; Pred. No. 0.051;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      Aspergillus niger alpha-amylase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVOZYMES AS.
(NOVO ) NOVOZYMES NORTH AMERICA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 35; Page 31-33; 33pp; English.
                                                                                                                                                                            AAE24207 standard; protein; 484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Veit C, Felby C, Fuglsang CC;
                                                                                                                                                                                                                                                                                                                                                                                                                       2000DK-00001676.
2000US-0252213P.
2000DK-00001854.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-2000; 2000US-0256015P
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                      Query Match
Best Local Similarity luv.
9; Conservative
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nes 8; Conservative
                                                                                                 94 AYHGYWQQD 102
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                                                                                                                                                                                                                                                                                Ethanol production;
fuel alcohol; fuel
                                                                                      1 AYHGYWQQD
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           Sequence 494 AA;
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                                                                                                                                                                                                      AAE24207;
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Matches
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enzyme; alcohol; slurry; water; granular starch; acid alpha-amylase;
glucoamylase; gelatinization; yeast; beer; fuel ethanol; potable ethanol;
industrial ethanol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for the production of an alcohol product by holding a slurry of water and granular starch in the presence of an acid alpha-amylase and a glucoamylase at 0-20 deg C below the initial gelatinization temperature of the granular starch, holding the slurry in the presence of acid alpha-amylase, glucoamylase and yeast at 10-35 deg C to produce ethanol; and optionally recovering the ethanol. The method is used for the production of an alcohol product such as beer or recovered ethanol, e.g. fuel ethanol, potable ethanol or industrial ethanol. This sequence represents an acid fungal alpha-amylase from Aspergillus niger used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Production of alcohol product, e.g. beer, comprises holding slurry of water and granular starch in presence of acid alpha-amylase and glucoamylase followed by simultaneous saccharification and fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
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100.0%; Pred. No. 0.64;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; SEQ ID NO 1; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB80178 standard; protein; 630 AA.
                                                                                                                                                                                                                                                                                            10-MAR-2004; 2004WO-DK000154
                                                                                                                                                                                                                                                                                                                                                 10-MAR-2003; 2003US-0453326P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                  Aspergillus niger.
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cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; malrodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability. Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, polygalacturonase; xylanase; gallate ester linkage; detergent; Bussey H; Claim 17; Page 139-40; 169pp; English. beverages, textiles and detergents. Roemer T, 05-AUG-2002; 2002WO-US024842. 03-AUG-2001; 2001US-0309870P N-PSDB; ABQ80347, ABQ80348 (ELIT-) ELITRA PHARM INC. Aspergillus fumigatus. Storms R, 2003-332729/31 WO2003012071-A2 13-FEB-2003 Jiang B, 

The sequences given in ABBB0164-87 show enzymatic proteins derived from A. funigatus. These proteins display the catalytic activity of an enzyme cuch as tennase, cellulase, glucose oxidase, glucoamylase, phytase, betagalactosidases, invertase, lipase, alpha-amylase, laccase, polygalactucnosnae or xylanase. Compositions comprising the tannase are useful for modulating the amount of cellulase in a composition and composition comprising cellulase are useful for modulating the amount of cellulase in a composition comprising glucose oxidase are useful for modulating the amount of cellulase are useful for modulating the amount of success or oxygen in a composition. Composition comprising betagase are useful for modulating the amount of laccose or oxygen in a composition. Composition comprising sucrase or invertase are useful for modulating the amount of laccose in a composition. Composition composit particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions Sequence 630 AA;

0; Gaps Length 630, 0; Indels DB 6; 53.8%; Score 7; DB 6 100.0%; Pred. No. 9.9 :ive 0; Mismatches 7; Conservative Query Match Best Local Similarity Matches 7; Conserv

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The peptides AAR84928-R85063 and AAR85786-R85842 are peptides derived from the WD40 regions of a range of proteins (AAR85851-R85893) containing WD40 (also called beta-transducin) amino acid repeat regions. The WD40 regions are involved in protein-protein interactions between proteins involved in intracellular signalling. An example of such an interaction is between protein kinase C and receptors of activated protein kinase (RACK), esp. RACK-I (AAR85850). The proteins were isolated based on homology with beta-transducin or with its WD-40 consensus sequence. The peptides can be used to identify target proteins contg. WD-40 motifs, as modulators of enzyme esp. isozyme, activity of proteins involved in protein-protein interaction and to screen for drugs that will affect protein-protein interaction involving WD-40 domains. This peptide is derived from the repeat II from the TUPI protein
                                                                                                                                                                                                                                                          WD40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signalling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the activity of a protein, eg. protein kinase C, which interacts with a protein contg. a WD-40 region.
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                                                                                                                                                                                                                          Peptide rII from the WD-40 domain-contg. TUP1 protein.
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100.0%; Pred. No. 11;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 271; 351pp; English.
                                                                                                                      AAR85808 standard; peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-US001210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00190802
                                                                                                                                                                                         13-SEP-1996 (first entry)
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                                102 YHGYWQQ 108
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                                                                                                                                                                                                                                                                                                                                                                    WO9521252-A2
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7, 2005, 19:15:40 ; Search time 1.58108 Seconds (without alignments) 791.116 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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283416 segs, 96216763 residues US-10-820-200-2\_COPY\_98\_110 Gapop 60.0 , Gapext 60.0 1 AYHGYWQQDIYSL 13 OLIGO Perfect score: Scoring table: Word size : Sequence: Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

a Query Score Match Length DB Result No.

Description

cyclomaltodextrin cyclomaltodextrin	cyclomaltodextrin	kallikrein (PK-120 ylmG protein [impo	conserved hypothet hypothetical prote	hine pho response	SOS response regul prophage pil prote ABC-transporter, A
A58800 S09196	ALBSGC ALBSGC	S50175 E95193	B99060 AF1183 AG1540	F97007 AF1237	AC1600 BB6801 F96955
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30 31 32	) W W c	3.66	8 8 8 8 9 9	4 4 1 2 2	<b>4 4 4</b> ይ <b>4</b> የ

## ALIGNMENTS

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C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe A;Reference number: A48305, MUID:90254827; PMID:2340591
A;Accession: A48305
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-498 «KOR»
C;Superialion: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes alpha-amylase; of internal 1,4-alpha-D-glucosidic bonds
C;Superfamily: Aspergillus alpha-amylase; hydrolase; polysaccharide degradation
C;Superfamily: Aspergillus alpha-amylase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology
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alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 13; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 13; Conservative 0; Mismatches 0;
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# 99 AYHGYWQQDIYSL 111

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A;Accession: S04548 A;Molecule type: DNA A;Residues: 1-499 <WIR> A;Cross-references: UNIPROT:P10529; EMBL:X12725; NID:g2430; PIDN:CAA31218.1; PID:g29592 A;Genetics: AMY1 A;Accession: A33214 Alpha-amylase (BC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
NyAlternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
Syspeciaes: Aspergillus oryzae
C;Speciaes: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C;Accession: S04548; A33214; JS0240; A91930; A93767; A10627
Mirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon
A;Reference number: S04548; MUID:89237897; PMID:2785629

A;Molecule type; mRNA A;Residudes: 1-499 «M12. A;Cross-references: GB:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921 R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

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Local Similarity 100.0%;
les 13; Conservative C
  A,Accession: A3315
A,Status: translation not shown
A,Molecule type: mRNA
A,Residues: 1-499 «WIZ>
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A, Residues: 1-499 <SHI>C, Function:
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A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing
A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: JS0240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: A93767
A,Molecule type: protein
A,Residues: 434-443.446-447,'Q',449-458,'GTTV',459-464,467-468,'B',470,'B',472-499 <NARX
R,Matesura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
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A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Contents: annotation; X-ray crystallography, 3.0 angstroms S.Swift, H.J.; Brady, L.,; Derwenda, Z.S.; Dodson, B.J.; Turkenburg, J.P.; Wilkinson, A. submitted to the Brookhaven Protein Data Bank, August 1992
A;Reference number: A51548; PDB:6TAA
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NAlternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
Sybercies: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
R;Mircel, S, Iachmund, A.; Mildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon A;Reference number: S04548; MUID:89237897; PMID:2785629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Structure and possible catalytic residues of Taka-amylase A. A;Reference number: A37454; WUID:84212370; PMID:6609921
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;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
;Genetics: <AMY2>
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                                                                                                            A; Molecule type: DNA
A; Residues: 1-499 <GEN>
A; Genetics: AMY2
A; Note: the authors refer to this as isozyme II
R; Isemura, S.; Ikonaka, T.
J. Biochem. 74, 1-10, 1973
A; Reference number: A91930; MUID:74001521; PMID:4733850
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A, Reference number: A93767
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Les 13; Conservative
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A; Molecule type: protein
A; Residues: 206-225 <ISE>
R; Narita, K.
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A,Residues: 1-499 <W]
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A;Cross-references: GB:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
R;Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin A;Reference number: JS0240; MUID:89378767; PMID:2789162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase; meta
F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 22-499/Product: alpha-amylase 3 #status experimental <MAT>
F; 194-321/Domain: alpha-amylase core homology <AMY>
F; 195-159, 171-185, 261-304, 461-496/Disulfide bonds: #status experimental
F; 142, 183, 196, 231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F; 218, 198, 198, 210, Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 211, 251, 318/Active site: His, Glu, Asp #status experimental
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Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expressio
A;Reference number: JS0663; MUID:92323146; PMID:1368777
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C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase estatus predicted <ALP>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Aspergillus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
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A; Residues: 1-499 «GEN»
A; Note: the authors refer to this as isozyme I
A; Matsuura, Y:; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A; Title: Structure and possible catalytic residues of Taka-amylase A.
A; Contents: annotation; X-ray crystallography, 3.0 angstroms
C; Comment: One atom of calcium per molecule is essential for activity.
C; Genetics:
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A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
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100.0%; Score 13; DB 1; I
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 13; Conservative 0; Mismatches 0;
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Cyaccession: B48305
R; Accession: B48305
R; Cour. Genet. 17, 203-212, 1990
A; Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe A; Accession: B48305
A; Accession: B48305
A; Accession: B48305
A; Cour. Genet. 17, 203-212, 1990
A; Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe A; Accession: B48305
A; Accession: B48305
A; Cour. Genet. Compared with conceptual translation
A; Molecule type: DNA
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C;Species: Aspergillus niger
C;Species: Aspergillus niger
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35282
R;Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pet Biochemistry 29, 6244-6249, 1990
A;Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom A;Reference number: A35282
A;Accession: A35282
A;Accession: A35282
A;Accession: A35282
A;Accession: A35282
A;Accession: A35282
C;Function:
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A; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;173-300/Domain: alpha-amylase core homology <AMY>
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                                                                                                                                                                                                                                                                                                                                   alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C.Species: Aspergillus awamori
C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
           Gaps
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100.0%; Pred. No. 3.2e-08;
ive 0; Mismatches 0;
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100.0%; Pred. No. 0.03;
:ive 0; Mismatches
       Mismatches
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C.Function:
                                                                                                                    99 AYHGYWQQDIYSL 111
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Best Local Similarity 100.
Matches 13, Conservative
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       13; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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       Matches
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                                                                                                                                                                                                                                                                                                                               C, Accession: JT0466
R, Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A; Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Punction:
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
C; Keywords: glycoprotein; glycosidase; hydrolase; signal sequence #status predicted <NGT>
F; 22,499/Product: alpha-amylase fartus predicted <NMT>
F; 21,499/Domain: alpha-amylase core homology <AMY>
F; 218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 231,251,318/Active site: His, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                       alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N;Alternate names: glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NiAlternate names: Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1-499 <TAD>
A;Cross-references: UNIPROT:P10529
C;Comment: See also PIR.JK0201 and PIR.JS0240.
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 13; DB 2; Length 499; 100.0%; Pred. No. 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N;Alternate names: Taka-amvlaco n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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AYHGYWQQDIYSL 111
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A; Accession: JT0466
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ses 13, Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA
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Matches
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Gaps

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A;Accession: 831478
A;Accession: BNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-482 <HOF>
A;Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:g48289; FIDN:CAA49465.1; FID:g4829
A;Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:g48289; PIDN:CAA49465.1; PID:g4829
C;Punction: Catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
A;Pathway: glycogen/starch degradation
C;Suporfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysacoharide degradation
F;194-319/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glysosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75392
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.; Shen, M.; Shen, M.; Shen, M.; Shen, M.; States, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75392
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: UNIPROT:Q9RUB8; GB:AE001991; GB:AE000513; NID:g6459223; PIDN:AAF110
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:013996; EMBL:298978; PIDN:CAB11675.1; GSPDB:GN00066; SPDB:S.
A;Experimental source: strain 972h-; cosmid c27E2
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T3848
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
A;Reference number: Z21749
A;Accession: T38448
A;Accession: T38448
A;Accession: T38448
A;Accession: T38448
A;Residues; Lealiminary; translated from GB/EMBL/DDBJ
A;Residues: 1-491 <MUR>
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A;Introns: 325/3; 476/3
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
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A;Map position: 1
C;Superfamily; Aspergillus alpha-amylase; alpha-amylase core homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.2%; Score 6; DB 2;
100.0%; Pred. No. 7.3;
rative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 6; Conservative
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A; Residues: 1-478 < RAM
A; Barrell, B.G.; Seeger, K.; Harris, D.
Bubmitted to the EMBL Data Library, April 1999
A; Reference number: 221976
A; Recession: T41181
A; Accession: T41181
A; Residues: translated from GB/EMBL/DDBJ
A; Residues: 1-203 < RAM
A; Residues: 1-204 < RAM
A; Residues: 1-205 < RAM
A; Residues: 1-205 < RAM
A; Residues: 1-205 < RAM
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submitted to the EMBL Data Library, December 1992
A;Description: The gene amyTV coding for a non-glucogenic alpha-amylase from Thermoactin
A;Reference number: 831478
C;Accession: T41560
K;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
Submitted to the EMBL Data Library, May 1998
A;Reference number: Z21991
A;Reference number: Z21991
A;Accession: T41560
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T4150
A;Residues: 1-429 <WOO>
A;Residues: 1-429 <WOO>
A;Residues: UNIPROT:074952; EMBL:AL023705; PIDN:CAA19267.1; GSPDB:GN00068; SPDB:A;Experimental source: strain 972h-; cosmid c736
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable alpha-amylase precursor SPCC11E10.09c - fission yeast (Schizosaccharomyces pomb C; Species: Schizosaccharomyces pombe C; Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004 C; Accession: T40860; T41181 R; Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, October 1999 A; Reference number: Z21952
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C;Species: Thermoactinomyces vulgaris
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Acession: S31478
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A;Map position: 3
A;Introns: 320/3; 468/3
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
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A;Map position: 3
C;Superfamily: phenylalanine-tRNA ligase alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
5. 6.6;
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| AYHGYW 94
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46.2%; Score 6; DB 2 100.0%; Pred. No. 7.6 Live 0; Mismatches

7, 2005, 19:33:47

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F;134,229/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                       Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Job time : 1.58108 secs
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C,Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C,Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C,Superfamily: Aspergillus alpha-amylase; alycoprotein; glycosidase; hydrolase; metall
F,1-26/Domain: signal sequence #status predicted <SIG>
F,27-494/Product: alpha-amylase #status predicted <MAT>
F,200-327/Domain: alpha-amylase core homology <AMY>
F,57-65,177-191,267-310,462-493/Disulfide bonds: #status predicted
F,148,189,202,237/Binding site: calcium (Asn, Gln, Asp, His) #status predicted
F,234/Binding site: carbohydrate (Asn) (covalent) #status predicted
F,233,257,324/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S00064
R;Itch, T.; Yamashita, I.; Fukui, S.
RSES Lett. 219, 339-342, 1987
A;Title: Nucleotide sequence of the alpha-amylase gene (ALP1) in the yeast Saccharomycop A;Reference number: S00064; MUID:87276512; PMID:3497057
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R;Claros, W.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
Curr. Genez, 24, 75-83, 1993
A;Title: Molecular structure of the SWA2 gene encoding an AWY1-related alpha-amylase fro
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A;Residues: 1-507 <CLA>
A;Cross-references: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g3965
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A;Cross-references: UNIPROT:P21567; EMBL:X05791; NID:94847; PIDN:CAA29233.1; PID:94848
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Thm
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C; Punction:
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C; Supeription: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase; polygaccharide degradation
C; Reywords: glycoprotein; glycosidase; hydrolase; polygaccharide degradation
C; 1-20/Domain: signal sequence #status predicted <MAT>
F; 1-50/Product: alpha-amylase #status predicted <MAT>
F; 205-332/Domain: alpha-amylase core homology <AMY>
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C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
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C;Species: Schwanniomyces occidentalis
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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Matches 6; Conservative 0; Mismatches
46.2%; Score 6; DB 2
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

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Gene 84:319-327(1989)
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                   Aspergillus oryzae.
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                                                                                                                                                                                                                                                                                           Aspergillus kawachi (Aspergillus awamori var. kawachi).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=40384;
         similarity).

Calcium 1 (By similarity).

Calcium 2 (By similarity).

Calcium 1 (via carbonyl oxygen) (By similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

By similarity.

By similarity.

By similarity.

By similarity.
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Calcium 1 (via carbonyl oxygen)
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Submitted (MAY-2003) to the EWBL/GenBank/DDBJ databases.
1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AB109452; BAD01051.1; -.
GO; GO:0004575; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IRR00641; Alpha amylast interPro; IRR00641; Alpha amylast sub.
InterPro; IRR00641; Alpha amylast sub.
Pfam; PR00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
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MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
TSukagoshi N., Purukawa M., Nagaba H., Kirita N., Tsuboi A., Udaka S.;
"Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
evidence for multiple related genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tada S., limura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.; "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus oryzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
Genes M.J., Dove M.J., Seligy V.L.;
"Aspergilus oryzae has two nearly identical Taka-amylase genes, each containing eight introns.";
Gene 79:107-117(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 206-225. MbMed=4733850; MBDLINE=74001521; PubMed=4733850; ISemura S., Ikenaka T.; "The amino acid sequences of glycopeptides obtained from Taka-amylase "The amino acid sequences of glycopeptides
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Mateunra Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
Toda H., Narita K., Kakudo M.;
"Molecular structure of taka-amylase A. I. Backbone chain folding at
Bukaryota, Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                     Wirsel S., Lachmund A., Wildhardt G., Ruttkowski E.; "Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon organization.";
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Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
"Structure and possible catalytic residues of Taka-amylase A.";
J. Biochem. 95:697-702(1984).
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Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
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                                                                                                                                                                           STRAIN-DSM 63303;
MEDLINE-89237897; PubMed-2785629;
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R EMBL; X12725; CAA1219.1; -
R EMBL; X12727; CAA12120.1; -
R EMBL; M33218; AAA32708.1; -
R PIR; JK0621; JT0466;
R PIR; JT0466; JT0466.
PIR; S04548; ALAS1.
R PDB; CTAA; X-ray; 0=22-499.
R PDB; CTAA; X-ray; 0=22-499.
R PDB; TTAA; X-ray; 0=22-499.
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INTERPO; IPRO06046; Glyco-hydro-13.
R PETMIS; PRO0110; ALPHAAMYLASE.
R SMART; SM00642; Aamy; 1.
PRINTS; PRO010; ALPHAAMYLASE.
R SMART; SM00642; Aamy; 1.
PRINTS; PRO010; Glyco-phydrate metabolism;
M Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
M Multigene family; Signal.
T SIGNAL
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Calcium 1 (via carbonyl oxygen).
Calcium 1.
Calcium 2.
Calcium 1 (via carbonyl oxygen).
Calcium 1 (via carbonyl oxygen).
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Q -> T (in Ref. 5).

D -> Y (in Ref. 3).

P -> L (in Ref. 3).

G -> V (in Ref. 3).

G -> H (in Ref. 3).

I -> L (in Ref. 5).

I -> L (in Ref. 5).

MPIY -> PYI (in Ref. 5).

G -> S (in Ref. 5).

S -> SD (in Ref. 5).
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Q -> R (in AMY3).
F -> L (in AMX3).
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MEDLINE=9223146; PubMed=1368777; Hara S.; Shibuya I., Tamura G., Ishikawa T., Hara S.; Saccharomyces cervelsiae., September and saccharomyces cervelsiae., September Shores Shore September Section Section Shore Section 
   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.; "Cloning, characterization, and expression of two alpha-amylase genes from Aspergillus niger var. awamori.";

Curr. Genet. 17:203-212(1990).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in Oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium is per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006646; Alpca, amyl_cat.
InterPro; IPR006646; Glyco, hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS, PR0010; Alpha-amylase.
SMART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase; Hydrolase; Multigene family; Properties
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Calcium 1 (By similarity).
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Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
By similarity.
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Nucleophile (By similarity).
Proton donor (By similarity)
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01-APR-1993 (Rel. 25, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
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                                                                                                                                                                                                Interpro; IPR006589; Alp amyl cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam, PF00128; Alpha-amylase; 1.
SMANTS; PR00110; ALPHAMYLASE.
SMART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
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Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5062;
[1]
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Calcium 1 (By similarity).

Calcium 2 (By similarity).

Calcium 1 (via carbonyl oxygen)

similarity).

Calcium 2 (By similarity).
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Proton donor (By similarity).
By similarity.
By similarity.
Calcium I (By similarity).
Calcium I (via carbonyl oxygen)
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01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
  99 AYHGYWQQDIYSL 111
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Matches 13; Conservative
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Aspergillus flavus.
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Name=amyA;
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                                                                                                            "Molecular cloning and characterization of a transcriptional activator gene, amyR, involved in the amylolytic gene expression in Aspergillus
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Biosci. Biotechnol. Biochem. 64:816-827(2000).
Biosci. Biotechnol. Biochem. 64:816-827(2000).
EMBL, AB021876; BAA95703.1;
PIR; NUOS88.
PIR; S04549; ALAS3.
HSSP, PI0529; 7TAA.
GO; GO:0004556; Falpha-amylase activity; IEA.
GO; GO:00018756; P:carbohydrate metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1011_TaxID=105351;
                   MEDLINE=20289310; PubMed=10830498;
Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
Iimura Y.;
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-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AB083159; BAD06002.1;
GO; GO:0004556; P:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006049; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_l3.
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100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels
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2B357AE38B36C1C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q76L99;
6-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   499 AA.
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006589; Alp_amyl cat_gub.
InterPro; IPR006046; Glyco hydro_13.
PFam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SWART; SM00642; Aamy; 1.
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PRINTS; PR00110; ALPHAAMYLASE.
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SEQUENCE 499 AA; 54794 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3lycosidase, Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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SEQUENCE FROM N.A.
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The State of Aspergillus flavus: Involvement in a flatoxin biosynthesis in maize kernels.";

The alpha-amylase gene of Aspergillus flavus: Involvement in a flatoxin biosynthesis in maize kernels.";

Thytopathology 89:908-914 (1999).

Therpro; IPR006049; Alpha-amylase activity, acting on glycosyl bonds; IEA.

Therpro; IPR006049; Alpha-amylase activity, acting on glycosyl bonds; IEA.

Therpro; IPR006049; Alpha-amylase activity.

Therpro; IPR006049; Alpha-amylase; 1.

Therpro; IPR00110; Alpha-amylase; 1.

Therpro; IPR00110; Alpha-amylase; 1.

Therpro; IPR00110; Alpha-amylase; 1.

Therpro; IPR00110; Alpha-amylase; 1.
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=5059,
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AF208225; AAF17103.1; --
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                                                                                    05-UUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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GO; GO:0005975; P::arbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Alpha_myl_cat_sub.
InterPro; IPR006046; Glyco_hydro_l3.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
499 AA
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15-701.1998 (Rel. 36, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                      Query Match 84.6%; Score 11; DB 2; Length 490; Best Local Similarity 100.0%; Pred. No. 0.00015; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA; 14950 MW; 2ACE8FDC55E79637 CRC64;
                                                                                                      SMART; SM00642; Aamy; 1.
SEQUENCE 490 AA; 54249 MW; A891C4ACEAEB5305 CRC64;
                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                    91 AYHGYWQQDIY 101
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ID AMYA ASPNG
AC P56271;
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Aspergillus kawachi (Aspergillus awamori var. kawachi).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=40384;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Kaneko A., Sakamoto Y., Tamura G., Ishikawa T., Ohba T.;
"Moleko A., Sudo S., Sakamoto Y., Tamura G., Ishikawa T., Ohba T.;
"Molecular-cloning and determination of the nucleotide-sequence of gene encoding an acid-stable alpha-amylase from Aspergillus-kawachii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUP1-like protein (Fragment).
Pichia angusta (Yeast) (Hansenula polymorpha).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes; Saccharomycetateses, Saccharomycetateses.
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                                                                                                                          0; Indels
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Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
EMBL, AB008370; BAA22993.1; -.
HSSP; P56271; 2AAA.
                                                        SIĞNAL 1 21 Potential.
SEQUENCE 634 AA; 69242 MW; 16COBEGAF6FBOE9B CRC64;
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                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Last annotation update)
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GO; GO: 000324; F:catalytic activity; IEA.
GO; GO: 000324; F:catalytic activity; IEA.
IO. GO: 0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006589; Alpha amyl cat.
InterPro; IPR002689; Alpha amyl cat.
Fram; PF00128; Alpha-amylase; 1.
Pram; PF00128; Alpha-amylase; 1.
Probom; PD001568; GBM 20; 1.
SMART; SM00642; Aamyl.
SEQUENCE 640 AA; 69507 MW; 676BF9D0236720DD CF
                                                                                               61.5%; Score 8; DB 2;
100.0%; Pred. No. 0.46;
tive 0; Mismatches
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100.0%; Pred. No. 0.46;
iive 0; Mismatches
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 Pfam; PF00686; CBM 20; 1.
ProDom; PD001568; Glyco hydro_CBD; 1.
SMART; SM00642; Aamy; 1.
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Best Local Similarity 100.vv
                                                                                 Query Match
Best Local Similarity 100.
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                                          Signal.
SIGNAL
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Q6Y198;
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Sukaryota, Pungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Burotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=105351;
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STRAIN=KT-11;
Matsubara T.;
Submitred (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB083162; BAD06005.1; --
EMBL; AB083160; BAD06003.1; --
HSSP; P04064; 1ACZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52935 MW; 04D596E34680656D CRC64;
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Last annotation update)
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GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0003975; P:carbohydrate metabolism; IEA.
InterPro; IPR006647; Alpha amyl_cat.
InterPro; IPR006589; Alp amyl_cat sub.
InterPro; IPR002044; GlyCo_hydro_GBD.
Fam; PF00128; Alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%; Score 8; DB 1;
100.0%; Pred. No. 0.38;
ive 0; Mismatches
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05-JUL-2004 (TrEMBLrel. 27, C.
05-JUL-2004 (TrEMBLrel. 27, L.
05-JUL-2004 (TrEMBLrel. 27, L.
Alpha-amylase precursor.
Name=amyl III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
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Megrayn T., Reilly K., Cipriani G., Murphy P., Newcomb R., Gardner R., MacRae E.; Anovel Japha-amylase gene is transiently upregulated during low macrae E.; Anovel Japha-amylase gene is transiently upregulated during low temperature exposure in apple fruit."; temperature exposure in apple fruit."; Eur. J. Biochem. 267:1313-1322(2000).

1. SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

EMBL; AF153828; AAF63239-1; -...

RSP; P04063; 1BG9.

RSP; P04063; 1BG9.

RO; GO:0016356; F:alpha-amylase activity; IEA.

GO; GO:0016378; F:hydrolase activity, acting on glycosyl bonds; IEA.

RO; GO:0016378; P:carbohydrate metabolism; IEA.

RITCEPPO; IPR006046; Glyco_hydro_lydro
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TREMBLrel. 24, Last annotation update)
Alpha-amylase (EC 3.2.1.1)
Malus domestica (Apple) (Malus sylvestris).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Rosales; Rosaceae; Maloideae; Malus.
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                                                                                                           Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

L. Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Contains 7 WD repeats.

R. Billiarity: Contains 7 WD repeats.

R. Filliarity: PRO0400; WD40.

R. PETAT, PRO0400; WD40.

R. PRINTS; PRO0400; WD40.

R. ROMORT; SM00320; WD40.6.

R. ROMART; SM00320; WD40.6.

R. ROMORT; PS000678; WD_REPEATS_1; 3.

R. ROSITE; PS000678; WD_REPEATS_2; 6.

R. ROSITE; PS00924; WD_REPEATS_REGION; 1.

R. ROSITE; PS00924; WD_REPEATS_REGION; 1.

R. NON_TER. 322 322
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322 AA; 35083 MW; 017CADD0E0E90B03 CRC64;
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SEQUENCE 413 AA; 46883 MW; C77763D797B6D0EA CRC64;
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100.0%; Pred. No. 52;
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MEDLINE=20156234; PubMed=10691968;
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Best Local Similarity 100.0
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NCBI_TaxID=4905;
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7, 2005, 18:24:00 ; Search time 3.75676 Seconds (without alignments) 954.162 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                    OM protein - protein search, using sw model
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US-10-820-200-2\_COPY\_161\_167 SSQDYFH 7 Title: Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot\_sprot:\*
2: uniprot\_trembl:\* 93:\* UniProt Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

Q96191 homo sapien O88277 rattus norv			0978k2 streptococc	Q7usul rhodopirell O8dz39 streptococc	Q8e4p7 streptococc	_	Q9cuh8 mus musculu	Q8eu15 oceanobacil	Q73156 treponema d
Q96L91 FAT2 RAT	Q6XYZ7 Q7RM89	AGH ARMVU Q9CÜQB	Q97SK2	Q7USU1 08DZ39	Q8E4P7	P97975	баслив	QBEU15	Q73L56
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33	32	322	32	32	32	32	32	32	32
32 33	3.4 3.5	36 37	38	39 40	41	42	43	44	45

### ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          NEDLINE-1074137;
MEDLINE-9024827; PubMed=2340591;
MEDLINE-9024827; PubMed=2340591;
MEDLINE-9024827; PubMed=2340591;
MEDLINE-9024827; PubMed=2340591;
Royer T.J., Hompson S.A., Ward M., Wilson L.J., Berka R.M.;
"Cloning, characterization, and expression of two alpha-amylase genes from Aspergillus niger var. awamori.";
Curr. Genet. 17:203-212(1990).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in Oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Multigene family; Signal.
                                                                                                                                                 Aspergillus awamori.
Bukaryota; Yungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
                                           25-CCT-2004 (Rel. 34, Last sequence update)
Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan Name=AMYA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-amylase A.
Nucleophile (By similarity).
Proton donor (By similarity).
By similarity.
Calcium 1 (By similarity).
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PIR; A48305; A48305.

HSSP; P10529; 77AA.

InterPro; IPR006589; Alp amyl_cat_sub.

InterPro; IPR006647; Alpha_amyl_cat.

InterPro; IPR066047; Alpha_amyl_cat.

Pfam; PF00128; Alpha_amylase; 1.

PRINTS; PR001100; ALPHAAMYLASE.
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                    PRT;
                    STANDARD;
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AMYA_ASPAW
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RESULT 2 Q76CT3

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SEQUENCE FROM N.A.
MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
TSUKAGOShi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Udaka S.;
"Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
evidence for multiple related genes.";
Gene 84:319-327(1989).
                                                                                                                                                                                                                                                                                                                                                                                           Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.; "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus oryzae."; Agric. Biol. Chem. 53:593-599(1989).
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-89378967; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
Genes M.J., Dove M.J., Seligy V.L.;
"Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing eight introns.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=74001521; PubMed=4733850; Isemura S., Ikenaka T.; "The amino acid sequences of glycopeptides obtained from Taka-amylase A with trypsin and chymotrypsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
BIZOZOWSKÍ A.M., Davies G.J.;
Structure of the Aspergillus oryzae alpha-amylase complexed with the inhibitor acarbose at 2.0-A resolution.";
Biochemistry 35:10837-10845(1997).
-!- CATALYITC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular structure of taka-amylase A. I. Backbone chain folding at 3-A resolution.";
J. Biochem. 87:1555-1558(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-80227691; PubMed-6156152;
Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
Toda H., Narita K., Kakudo M.;
                                   Aspergillus oryzae.
Bukaryota, Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales, Fungi, Ascomeces, mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                 STRAIN=DSM 63303;
MEDLINE=89237897; PubMed=2785629;
Wirsel S., Lachmund A., Wildhardt G., Ruttkowski E.;
"Three alpha-amylase genes of Aspergillus oryzae exhibit identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
MEDLINE=84212370; PubMed=6609921;
Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
"Structure and possible catalytic residues of Taka-amylase A.";
J. Biochem. 95:697-702(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 22-499.
Toda H., Kondo K., Narita K.;
The complete amino acid sequence of Taka-amylase A.";
Proc. Jpn. Acad., B. Phys. Biol. Sci. 58:208-212(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975)
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                                                                                   NCBI_TaxID=5062;
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                   Name=AMY3:
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P10529; P11763; Q00250;
01-OCT-1989 (Rel. 12, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus kawachi (Aspergillus awamori var. kawachi).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=40384;
            similarity).
Calcium 1 (By similarity).
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
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Calcium 1 (via carbonyl oxygen)
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
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6-JUL-2004 (TrEMBLrel. 27, Created)
65-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 11;
ive 0; Mismatches 0;
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498 AA;
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                                                                                                                                                   DISULFID
                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                     DISULFID
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AMYA ASPOR
AC AMYA ASPOR
DT 01-0CT.
DT 25-0CT.
DE Alpha-1
GN Name=Al
GN Name=Al
GN Name=Al
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Matches

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SEQUENCE FROM N.A.
STRAIN=UVKL43F;
MEDLINE=0254827; PubWed=2340591;
Korman D.R., Bayliss P.T., Barnett C.C., Carmona C.L., Kodama K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus awamori.
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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01-0CT-1996 (Rel. 34, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Alpha-amylase B precursor (RC 3.2.1.1) (1,4-alpha-D-glucan Name=AMYB;
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     AMYB ASPAW
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D 10-007-

D 25-007-

D 25-007-

D 3-007-

D 3-007-

C NOBL

C NO
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch)
-1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations.
-1- SUBUNIT: Monomer.
-1- SIQUENTI: Monomer.
-1- BIOTECHNOLOGY: Used in the brewing industry to increase the fermentability of beer worts (including those made from unmalted cereals), in the starch industry to make high maltose and high DE syrups (starch saccharification), in the alcohol industry to reduce fermentation time, in the cereal food industry for Flour supplementation and improvement of chilled and frozen dough, and in the forestry industry for low-temperature modification of starch. Sold under the name Fungamyl by Novozymes.
-1- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
-1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SM00642; Aamy; 1.

3D-structure; Calcium-binding; Carbohydrate metabolism;
Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
Multigene family; Signal.
SIGNAL.
CHAIN. 22 499 Alpha-amylase A.
ACT SITE 227 Nucleophile.
ACT SITE 221 Proton donor.
ACT SITE 318 318 318
METAL 142 Calcium 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium 1.
Calcium 1 (via carbonyl oxygen).
Calcium 1.
Calcium 2.
Calcium 2.
Calcium 1.
Calcium 1.
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/FIG=CAR_000125.
F - L (in AMY3).
F - L (in AMY3).
TT -> DC (in Ref. 5).
O -> T (in Ref. 5).
O -> Y (in Ref. 3).
P -> L (in Ref. 3).
G -> V (in Ref. 3).
I -> L (in Ref. 3).
I -> L (in Ref. 3).
I -> L (in Ref. 5).
I -> L (in Ref. 5).
G -> A (in Ref. 5).
I -> L (in Ref. 5).
G -> A (in Ref. 5).
G -> A (in Ref. 5).
G -> S (in Ref. 5).
S -> SD (in Ref. 5).
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Gaps

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SEQUENCE FROM N.A.
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                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus shirousami.
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
[1]
                                                                                                                                                                                                                                                                                                                                       Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
By similarity.
N-linked (GlCNAC. . .) (Potential).
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Proton donor (By similarity).
By similarity.
By similarity.
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan Name-AMY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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740B96B11BC01A8A CRC64;
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InterPro; IRR006589; Alp amyl_cat_gub.
InterPro; IRR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
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Matches 7; Conservative
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499 AA;
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P30292;
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GN Name=

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Gaps
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Eukaryota; Pungl; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
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Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
By similarity.
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Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen)
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Nucleophile (By similarity).
Proton donor (By similarity).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Taka-amylase A (EC 3.2.1.1).
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InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54852 MW;
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218 2
499 AA;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylase (BC 3.2.1.1).
                                                                   499 AA
                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00110; ALPHAAMYLASE
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nes 7; Conservative
                                                                 PRELIMINARY;
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 162 SSQDYFH 168
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                                                                                                                                                                Aspergillus flavus
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Q01117;
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                                                                 "Molecular cloning and characterization of a transcriptional activator gene, amyR, involved in the amylolytic gene expression in Aspergillus
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Bukaryota, Pungi, Ascomycota, Pezizomycotina, Burotiomycetes;
Burotiales, Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                      Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
Iimura Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: Belongs to family 13 of glycosyl hydrolases. EMBL, AB08159; BAD06002.1; -. GO; GO:00045159; BAD06002.1; -. GO; GO:0004556; F:alpha-amylase activity; IEA. GO; GO:0005975; P:carbohydrate metabolism; IEA. InterPro; IPR006047; Alpha_amyl_cat. sub. InterPro; IPR006049; Alpha_amyl_cat_sub. InterPro; IPR006046; Glyco hydro.13. PF00128; Alpha-amylase; 1.
                                                                                                       Biosci. Biotechnol. Biochem. 64:816-827(2000).
-!-SIMULARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL, ABO21876; BAA95703.1; -.
PIR, JUN0588; JUN0588.
PIR, S04549; ALAS3.
HSSP; P10529; 7TAA.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0016798; F:hydrolase activity, acting on glycosyl bone
                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 40; DB 2; Length 499; Best Local Similarity 100.0%; Pred. No. 11; Matches 7; Conservative 0; Mismatches 0; Indels
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL 1 21 Potential.
SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;
                                                                                                                                                                                                                                                                                                                                499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;
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Last sequence update)
Last annotation update)
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InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR006046; Glyco hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
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                         MEDLINE=20289310; PubMed=10830498;
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SMART; SM00642; Aamy; 1.
Glycosidase; Hydrolase.
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SMART; SM00642; Aamy; 1.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity 100.0
Matches 7; Conservative
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SEQUENCE FROM N.A.
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Gaps
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"Amy1, the alpha-amylase gene of Aspergillus flavus: Involvement in aflatoxin blosynthesis in maize kernels.";
Phytopathology 89:908-94(1999).
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AF139925; AAF14264.1; -.
GO; GO:0004556; Falpha-amylase activity; IEA.
GO; GO:0016798; Fihydrolase activity, acting on glycosyl bonds; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=IGC4052B; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0; MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;
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"Cloning, sequence analysis and expression in yeasts of a CDNA containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";
Gene 166:65-71(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Lipomycetaceae, Lipomyces.
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10-0CT-2003 (Rel. 42, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan Name-LKA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indela
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InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR006046; Glyco hydro 13.
Pfam; PF00128; Alpha-amylase; 1.
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MEDLINE=96132108; PubMed=8593683;
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311 SSQDYFH 317
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                            SEQUENCE FROM N.A.
     NCBI_TaxID=29829;
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Matches
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Matches
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Q7RL16
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Characterization of a novel alpha-amylase from Lipomyces kononenkoae and expression of its gene (LKA1) in Saccharomyces cerevisiae.";
Curr. Genet. 28:526-533(1995).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
Linkages in Oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
-!- SUBCELLUAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
-!- SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                 EMBL; U30376; AAC49622.1; ALT_INIT.

PIR; JC4510; JC4510.

HSSP; P10529; 77AA.

InterPro; IPR006589; Alp amyl_cat_sub.

InterPro; IPR006689; CBM 21.

InterPro; IPR00128; Alpha amyl_cat.

Pfam; PF03170; CBM 21; 1.

Pfam; PF03170; CBM 21; 1.

SMART; SM00642; Aamy; 1.

Calcium-binding; Carbohydrate metabolism; Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity.
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
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Lipomyces starkeyi.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Lipomycetaceae; Lipomyces.
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N-linked (GlcNAc. . .) (Potential)
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Carbohýdrate binding type-21.
Nucleophile (By similarity).
Proton donor (By similarity).
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By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
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05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity 100...
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185
311
430
622
304
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353
377
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624 AA;
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ACT SITE
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SEQUENCE
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                                                                                                                      "Cloning and expression of Lipomyces starkeyi alpha-amylase in Escherichia coli and determination of some of its properties."; FEMS Microbiol. Lett. 233:53-64 (2004).
EMBL; AXISS-633 AAN75021.1; -.
HSSP; P26827; 1A47.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha_amyl_cat_sub.
InterPro; IPR005036; Alp amyl_cat_sub.
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

NCBI_TaxID=323;
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STRAIN=KSM 22M;
PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
Moon T.-W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 2; Length 647; 100.0%; Pred. No. 15; cive 0; Mismatches 0; Indels
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Fanelli V., Finetti-Sialer M., Gallitelli D.;
Fanelli V., Finetti-Sialer M., Gallitelli D.;
Fanelli V., Finetti-Sialer M., Gallitelli D.;
Falli, AJ604607-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ604607-2003) to the EMBL/GenBank/DBJ databases.
GO; GO:000524; F:ATP-dependent helicase activity; IEA.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Drosophila melanogaster CG11926 gene product, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70957 MW; D946071DB7560144 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative helicase.
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85.7%; Pred. No. 19;
iive 1; Mismatches
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Nature 430:35-44(2004).
EMBL; CR380957; CAG61198.1; -.
InterPro; IPR002013; Syja_N.
Pfam; PF02383; Syja_N; 1.
PROSITE; PS50275; SAC; 1.
SEQUENCE 627 AA; 71471 MW;
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5 SSQDWFH 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre B., Falrhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Zeniou-Meyer M., Zavanovic I., Bolocin-Fukuhara M., Thierry A., Zeniou-Meyer M., Zavanovic I., Bolocin-Fukuhara M., Thierry A., Bolchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Shallom J.D., Yoo, M., Cosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Ricdmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoashi A., Cumings L.M., Florens L., Yates P.R. III, Raine J.D., Sinden R.E., Harris M.A., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Frager C.M., Hoffman S.L., Gardner M.J.,
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Candida glabrata CBS138.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data. EMBL, AABLO1000756; EAA22214.1; -. InterPro; IPR004353; Yeast73DUF.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome K complete sequence.
                                     Plasmodium yoelii yoelii.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 36; DB 2; Length 596; 85.7%; Pred. No. 87; 1: Mismatches 0; Indels
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SEQÜENCE 596 AA, 69216 MW; 8170C2D33F53117D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01546; YEAST73DUF.
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                    SEQUENCE FROM N.A.
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                             lame=PY02732;
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Q6FNF7
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STRAIN-Portland;
Sekyere E.O., Edwards M.R., Stewart T.S., Schofield P.J., Knodler L.;
Sekyere E.O., Edwards M.R., Stewart T.S., Schofield P.J., Knodler L.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, API44322, AAD28486.1;
Plant, PF00023; ANK.
PFam, PF00023; ANK.
PRINTS, PRO1415; ANKYRIN.
SMART; SM00248; ANK; 3.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-WB C6;
Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
Uraft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-:- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                              GLP 456 15756 18038.
Giardia lamblīa ATCC 50803.
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
NCBI_TaxID=184922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ankyrin-like protein.
Giardia lamblia (Giardia intestinalis).
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
                                      Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 760;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.

EMBL; AACB01000038; EAA40649.1; -.
InterPro; IPR002110; ANK.
Pfam; PF00023; Ank; 3.
PRINTS; PR0415; ANKYRIN.
SEQUENCE 760 AA; 85474 MW; A01440ACE754099C CRC64;
627 AA; 71471 MW; DEAOB02466F4F480 CRC64;
                                                                                                                                                                                                                                                                                    01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2; I
Pred. No. 1.8e+02;
                                  Score 36; DB 2;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         760 AA
                                                                          1; Mismatches
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                                      90.0%;
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              Query Match
Best Local Similarity 85.73,
6; Conservative
                                                                                                                                                                                                                                                  PRELIMINARY;
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SQ SEQUENCE 760 AA; 85542 MW; 12E54841019CD475 CRC64;	Query Match Best Local Similarity 85.7%; Pred. No. 1.88+02:	Mismatches 0; Indels
85542 MW;	87.5%;	vative 1;
760 AA	Similarity	6; Consei
SQ SEQUENCE	Query Match Best Local	Matches

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Search completed: November 7, 2005, 18:52:32 Job time : 5.75676 sec8

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/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\* Minimum Match 0% Maximum Match 100% Listing first 45 summaries Issued\_Patents\_AA:\*

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing:

Database :

513545 seqs, 74649064 residues

Searched:

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 10, Appli Sequence 10, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 22820, A Sequence 2820, A Sequence 4016, Ap Sequence 4170, Ap Sequence 34772, A Sequence 49989, A Sequence 924, App 21, Appl 4, Appli 6538, Ap 5895, Ap 23, Appl 6596, Ap 10404, A Description Sequence US-08-339-715A-7 US-08-600-90BA-10 US-08-683-838A-10 US-09-182-859-7 US-09-672-459-7 US-09-636-252A-10 US-10-186-042-7 US-09-638-252A-10 US-09-248-796A-22820 US-09-583-110-4016 US-09-107-433-4442 US-08-616-392C-4 US-09-107-532A-6538 US-09-134-000C-5895 US-09-198-452A-924 US-09-438-185A-858 US-09-081-385-148 US-10-144-198-12 -09-270-767-34772 -09-270-767-49989 US-09-949-016-6596 US-09-949-016-10404 US-09-328-352-4170 US-08-700-359-21 -08-380-182-23 US-08-720-899-7 US-08-459-610-7 US-08-343-804-7 SUMMARIES Query Match Length DB 474 1000.0 11000.0 Score Result š

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Gapa

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Query Match 100.0%; Score 40; DB 1; Length 478; Best Local Similarity 100.0%; Pred. No. 4.7; Matches 7; Conservative 0; Mismatches 0; Indels

LENGTH: 478 amino acids TYPE: amino acid STRANDEDNESS: Bingle TOPOLOGY: linear

US-08-720-899-7

41, Appl 41, Appl 75, Appl 75, Appl 75, Appl 75, Appl 75, Appl		America, Inc.
sednence sed		5753460th Ame
25 1 US-08-485-455D-41 25 2 US-08-481-130C-41 25 3 US-08-481-211C-41 25 3 US-08-906-769-41 25 3 US-08-906-616-41 25 3 US-08-906-616-41 25 3 US-08-917-795-41 25 3 US-08-917-795-41 25 3 US-09-912-431-41 25 3 US-09-912-431-41 25 3 US-09-912-627-41 25 4 US-08-917-675-64 2 US-08-482-130C-75 64 2 US-08-482-13C-75 64 3 US-08-906-616-75 64 3 US-08-906-616-75 64 3 US-08-906-616-75 64 3 US-08-906-616-75	ALIGNMENTS	1.20-899-7  uence 7, Application US/08720899  uence 7, Application US/08720899  NERAL INFORMATION:  APPLICANT: Bisgaard-Frantzen, Henrik APPLICANT: Borchert, Torben Vedel APPLICANT: Wordeen, Allan APPLICANT: Van der Zee, Pia CITY: New York COUNTRY: USA ZIP: New York COUNTRY: USA ZIP: 10174-6401 COMPUTER READABLE FORM: WEDIUM TYPE: Floppy disk COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Batentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US 08/343,804 FILING DATE: 10-0CT-1996 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: US 08/343,804 FILING DATE: 10-0CT-1996 FILING DATE: 10-0CT-1996 FILING DATE: 12-807-0123 TELECOMMUNICATION NUMBER: 31,274 REGISTRATION NUMBER: 31,274
330 75.0 330 75.0 340 75.0 350 75.0 350 75.0 350 75.0 350 75.0 350 75.0 350 75		Pplica Say460 Bisg Borc Sver Thel Thel Thel Thel Thel Thel Thel Thel
00000000000000000000000000000000000000		NESULT 1 US-08-720-899-7 Sequence 7, Appl Patent No. 57534 GRNERAL INFORMAR APPLICANT: B APPLICANT: B APPLICANT: T CONDENTER: C CONPUTER: C COMPUTER: C C COMPUTER: C C C C C C C C C C C C C C C C C C C

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,715A
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/319,715A
RICHARDICATION NUMBER: US/08/319,715A
APPLICATION NUMBER: US/08/319,715A
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
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hes 7; Conservative
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                            STREET: 405
                                                                                                                             New York
                                                                                                                                                                 USA
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ADDRESSEE:
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STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10114-6401

COUNTRY: USA

ZIP: 10114-6401

COMPUTER: READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,610

FILING DATE: 02-UTN-1995

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION BATE:

APPLICATION: UNMBER: US 08/343,804

FILING DATE: 22-NOV-1994

ATTORNEY AGENT INFORMATION:

ANTORNEY AGENT INFORMATION:

ANTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
APPLICANT: Van der Zee, Pia
APPLICANT: Van See, Pia
APPLICANT: Van 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lowney Dr., Karen A.
REGIGSTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
APPLICANT: Van der Zee, Pia
APPLICANT: Van der Zee, Pia
CORRESPONDENCE: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  US-08-459-610-7; Sequence 7, Application US/08459610; Patent No. 5801043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08343804
Patent No. 5830837
GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 7; Conservative
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    1 SSQDYFH 7
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E: No. 58308370 No. 5830837disk of No. 5830837th America, Inc. 405 Lexington Avenue, 64th Floor
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APPLICANT: Kaneko, Hiroki
APPLICANT: Stadad, Toshikazu
APPLICANT: Shimada, Jiro
APPLICANT: Shaase, Michiyo
APPLICANT: Yanase, Michiyo
APPLICANT: Takata, Hiroki
APPLICANT: Takata, Hiroki
APPLICANT: Okada, Shigetaka
ITILE OF INVENTION: WETHOD OF ALTERING ENZYMES AND A NOVEL
ITILE OF INVENTION: WEOPULULANASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: DS/08/343,804
FILING DATE: 22-NOV-1994
CLASSIFICATION NUMBER: 3155
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REGISTRATION NUMBER: 31,274
REGISTRATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/08339715A
; Patent No. 5965442
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TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                          141 SSQDYFH 147
    1 SSQDYFH 7
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STREET: 405
                                                                                                        RESULT 6
US-08-683-838A-10
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Sequence 10, Application US/08600908A
Fatent No. 5989169
GENERAL INFORMATION:
APPLICANT: Brocher, Allan
APPLICANT: Brocher, Torben Vedel
TITLE OF INVENTION: 'Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESCENDENCE ADDRESS:
ADDRESSE: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
STREET: New York
STATE: New York
STATE: New York
STATE: New York
STATE: Now York
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100.0%; Score 40; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                     NAME: Melser, Allen S.
REGISTRATION NUMBER: 27,215
REFERENCE/DOCKET NUMBER: 18335
TELEPOMUNICATION INFORMATION:
TELEPHONE: 202-824-8199
TELEX: 248516
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Lag 7; Conservative
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                      STATE: New TOTK
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATENIN Release #1.0, Version #1.30
SOFTWARE: PatentIN Release #1.0, Version #1.30
SOFTWARE: PatentIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/683,838A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE:
ILING DATE: 13-FBB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Blagard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REPERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT FILING DATE: 1998-10-29
FBARLIER APPLICATION NUMBER: 0515/96
FBARLIER FILING DATE: 1996-04-30
Sequence 10, Application US/08683838A
Fatent No. 6022724
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TILLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
RELECOMMUNICATION INFORMATION:
TELLEPHONE: 212-867-0123
TELLEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
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amino acid
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Best Local Similarity 100.
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Sequence 22820, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION UNMBER: US/09/248,796A
CURRENT FILING DATION NUMBER: US 60/074,725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-186-042-7; Sequence 7, Application US/10186042; Patenn No. 6642044; Patenn No. 664204; GENERAL INFORMATION: APPLICANT: Svendsen, Allan; APPLICANT: Borchert, Torben APPLICANT: Bisgard-Frantzen, Henrik; TITLE OF INVENTION: Alpha-Amylase Mutants; FILE REFERENCE: 4796.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 10.204-00-02-06-28
PRIOR APPLICATION NUMBER: US/10/186,042
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1998-10-29
PRIOR PLILNG DATE: 1996-04-30
PRIOR PELING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0515/96
PRIOR PLILNG DATE: 1996-06-28
PRIOR PLILNG DATE: 1996-06-28
PRIOR PLILNG DATE: 1996-06-28
PRIOR PLILNG DATE: 1996-07-11
PRIOR PLILNG DATE: 1996-07-11
PRIOR PLILNG DATE: 1996-07-11
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus licheniformis US-10-186-042-7
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10
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                                                                                                                            SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 3; Length 478; 100.0%; Pred. No. 4.7; ive 0; Mismatches 0; Indels
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Sequence 10, Application US/09636252A
Sequence 10, Application US/09636252A
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Blsgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
ITILE OF INVERTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Svendeen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Busgard-Frantzen, Henrik
ITILE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 05/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1998-0-29
PRIOR PILING DATE: 1998-0-4-30
PRIOR PILING DATE: 1996-0-29
PRIOR PILING DATE: 1996-0-11
                  EARLIER FILING DATE: 1996-06-28

EARLIER APPLICATION NUMBER: 0775/96

EARLIER FILING DATE: 1996-07-11

EARLIER FILING DATE: 1996-11-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PastSEQ for Windows Version 3.0

LENGTH: 478
                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 SSODYFH 147
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Gaps
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APPLICANT: SUGIMOTO, WASAKAZU
APPLICANT: SUZUKI, TOMOKO
APPLICANT: SUZUKI, TOMOKO
APPLICANT: TANAKA, AKIKO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFPERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 95; 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051533
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8077
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 4442:
SEQUENCE CHARACTERISTICS:
LIENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.0%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 32; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LÕCATION 1...95
SEQUENCE DESCRIPTION: SEQ ID NO: 4442:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS TEXT EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,359
FILING DATE: 08-OCT-1996
CLASSIFICATION ATA:
APPLICATION NUMBER: JP-35019
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 21, Application US/08700359; Patent No. 5766925; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NORMAN F. OBLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 QDYFH 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 QDYFH 7
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US-08-700-359-21
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APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
PRIOR SELING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-13
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
THERAPEUTICS
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 40;
1; Mismatches 0; Indels
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28;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Pred. No.
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22820
LENGTH: 180
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
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US-09-107-433-4442
Sequence 4442, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
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Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptococcus pneumoniae US-09-583-110-4016
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STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                  ; ORGANISM: Candida albicans
US-09-248-796A-22820
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102 NQDYFH 107
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                                                                                                                                              TYPE: PRT
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Sequence 4, Application US/08616392C

Patent No. 5998165

GENERAL INFORMATION:
APPLICANT: Goold, Richard D.
APPLICANT: Gollamer, Jeffrey
APPLICANT: Coleman, Roger POLYNUCLEOTIDES PANCIA
TITLE OF INVENTION: AND PANCIB ASSOCIATED WITH PANCREATIC CANCER
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
COUNTY: USA
ZID.
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.3e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: usa

ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,392C
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/581,240
FILING DATE: 29-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acide
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TYPE: IMPREDIATE SOURCE:
LIBRARY: hNT
REGISTRATION NUMBER: 24,618

REFRENCENCY TOURSER: 10-819-0 PCT
FILECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2200
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
US-08-700-359-21
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         || ||:|
133 SSMDYYH 139
                                                                                                                                                                                                                                                                                                                                                               1 SSQDYFH 7
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Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                    2005, 18:11:05 ; Search time 3.7973 Seconds (without alignments) 771.303 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Sequence 10, Sequence 7, Al Sequence 7, Al Sequence 7, Al Sequence 10,
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Sequence 2
Sequence 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

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8: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US106_NEW_PUB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/US106_NEW_PUB.pep:*

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15: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US106_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-184-771-10
US-10-186-042-7
US-10-644-187-7
US-10-926-720-10
US-11-064-196-10
US-11-064-196-10
US-10-815-495-22
US-10-815-495-30
US-10-815-495-30
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                                                                                                                                                                                                                                                                                                                                                         1867879 segs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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40
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Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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length: 2000000000
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Match
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Maximum DB seq
                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                           Run on:
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Sequence 140941, Sequence 275630, Sequence 8854, Ap Sequence 8854, Ap Sequence 167129, Sequence 187129, Sequence 1442, Ap Sequence 271310, Sequence 271310, Sequence 496, Ap Sequence 496, Ap Sequence 496, Ap Sequence 4, Appli Sequence 686, Appli Sequence 1079, Appli Sequence 686, Appli Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42805, A
Sequence 74838, A
Sequence 75391, A
Sequence 75391, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, App.
Sequence 136212,
                                                                                                           Sequence
Sequence
                                                       Sequence
                                                                                             Sequence
S US-10-797-393A-5
7 US-10-877-849-40
8 US-10-849-40
8 US-10-228-063-45
8 US-10-228-063-45
8 US-10-228-063-45
8 US-10-228-063-81-6
8 US-10-424-599-218859
8 US-10-425-115-275630
1 US-09-970-944-20
1 US-09-970-944-20
1 US-09-970-944-20
1 US-09-970-944-20
1 US-09-970-944-20
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8 US-10-284-15-37310
9 US-10-285-15-37310
9 US-10-285-15-37310
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US-10-282-122A-42805
US-10-282-122A-74838
US-10-282-122A-75391
US-10-272-107-3
US-10-699-395-3
US-10-437-965-136212
US-10-153-668-104
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### ALIGNMENTS

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                                                                                                                                                                              Length 476;
Indels
                                                                                                                                                                             100.0%; Score 40; DB 17;
100.0%; Pred. No. 21;
ive 0; Mismatches 0;
                                                                                                                                                                                     Similarity 100.0%; P 7; Conservative 0;
                                                                                                                              TYPE: PRT
ORGANISM: Aspergillus oryzae
                                                                                                                                            FEATURE:
NAME/KEY: mat peptide
LOCATION: (1)..(476)
US-10-877-849-43
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Gaps

141 SSQDYFH 147

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RESULT 5
US-10-926-720-10
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Best Local Similarity 100.0%; Pred. No. 21; Length 478;
Matches 7; Conservative 0; Mismatches 0; Indels
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Publication No. US20030171236A1

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bridgerd-Frantzen, Henrik
ITIE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1996-04-30

PRIOR FILING DATE: 1996-04-30

PRIOR FILING DATE: 1996-04-30

PRIOR FILING DATE: 1996-04-30

PRIOR FILING DATE: 1996-07-11

PRIOR FILING DATE: 1996-11-08

NUMBER OF SEQ ID NOS: 37

SEQ ID NOS: 37

FUNDANT: 7
RESULT 2
US-10-184-771-10

Sequence 10, Application US/10184771
PUBLICATION NO. US20030170769A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE REPERENCE: 0776/1216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
PRIOR PRILOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEGOTUROR 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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141 SSQDYFH 147
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ORGANISM: A. oryzae
US-10-184-771-10
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US-10-186-042-7
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Sequence Application 89/10644187

Sequence Application 89/10644187

APPLICANT: Sender, Alian
APPLICANTOR A
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FILE REFERENCE: 0776/1F216-US2
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                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: A. oryzae
US-11-064-196-10
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REPERENCE/DOCKET NUMBER: 4394.204-US TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10980759; Publication No. US20050118695A1; GENERAL INPORMATION: APPLICANT: Svendsen, Allan APPLICANT: Borchert, Torben APPLICANT: Bisgard-Frantzen, Henrik TITE OF INVENTION: Alpha-Amylase Mutants FILE REFERENCE: 4796.204-US CURRENT FILING DATE: 2004-11-03; FRIOR PILING DATE: 2004-11-03; PRIOR PILING DATE: 1998-10-29; PRIOR PILING DATE: 1996-06-28; PRIOR PILING DATE: 1996-06-28; PRIOR PILING DATE: 1996-06-28; PRIOR PILING DATE: 1996-06-28; PRIOR PILING DATE: 1996-07-11; PRIOR PILING DATE: 1996-07-11; PRIOR PILING DATE: 1996-07-11; PRIOR PILING DATE: 1996-11-08; NUMBER OF SEQ ID NOS: 37; SOQ ID NO 75 SEQ ID NOS: 37; LENGTH: 478
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
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1. Sequence 10. Application US/11064196

5. Publication No. US20050170487A1

6. GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: BISGATC-Frantzen, Henrik

APPLICANT: BOSTCH-Frantzen, Vedel

7. TITLE OF INVENTION: Alpha-Amylase Mutants
                                                                                                                         LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
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; ORGANISM: Bacillus licheniformis
US-10-980-759-7
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Best Local Similarity 100...
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Sequence 22, Application US/10815495
Publication No. US20040191864A1
GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Matiah
TITLE OF INVENTION: MATIANTS OF Aspergillus Niger
FILE REPERENCE: 10345.200-US
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT PILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
SEQ ID NO 22.
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APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants; FILE REFERENCE: 5835.200-US; CURRENT FILING DATE: 2004-04-07; PRIOR APPLICATION NUMBER: US/10/820,200; PRIOR PILING DATE: 2004-11-09; PRIOR PLLING DATE: 2000-11-09; PRIOR FILING DATE: 1999-11-16; NUMBER OF SEQ ID NOS: 5; SOFTWARE: Patentin version 3.2; SEQ ID NO 2
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CURRENT APPLICATION NUMBER: US/11/064,196
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
SUTMER OF SEQ ID NOS: 16
SOFTWARE: FASELSEQ for Windows Version 3.0
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; ORGANISM: Aspergillus niger
US-10-815-495-22
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APPLICANT: Taira, Rikako
APPLICANT: Tragi, Shinobu
APPLICANT: Tragi, Shinobu
APPLICANT: Allain, Eric
APPLICANT: Hjort, Carsten
APPLICANT: Vikso-Nielsen, Anders
TITLE OF INVENTIVE HYBLID ENZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490.500-US
CURRENT APPLICATION NUMBER: US/10/877,849
                                                                                                                                                                  APPLICANT: Olsen, Hans Sejr
APPLICANT: Olsen, Hans Sejr
APPLICANT: Pedersen, Sven
APPLICANT: Pestersen, Rikke Monica
APPLICANT: Pestersen, Rikke Monica
TITLE OF INVENTION: ALCOHOLD PRODUCT
FILE REFERENCE: 10391.200-US
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 5:
LENGTH: 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-877-849-40

Sequence 40, Application US/10877849
Publication No. US20050054071A1
GENERAL INFORMATION:
                                                                                    US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Aspergillus oryzae US-10-797-393A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 100.
Matches 7; Conservative
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  162 SSQDYFH 168
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSODYFH 7
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hes 7; Conserv
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US-10-877-849-36
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Sequence 18, Application US/10815495
Publication No. US20040191864A1
GENERAL INFORMATION:
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Mutants Of Aspergillus Niger
TITLE OF INVENTION NUMBER: US/10/815,495
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 499
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                                                                                                         100.0%; Score 40; DB 16; Length 498; 100.0%; Pred. No. 22; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 40; DB 17; Length 498; 100.0%; Pred. No. 22; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/10877849
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Taira, Rikako
; APPLICANT: Taira, Rikako
; APPLICANT: Taira, Shinobu
; APPLICANT: Hjort, Carsten
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikeo-Nielsen
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH
; TITLE OF INVENTION: HYBRID ENZYMES
; TITLE OF INVENTION: HYBRID ENZYMES
; TITLE OF INVENTION: HYBRID S.00-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 30
; LENGTH: 498
; TURNENT HAS
; LENGTH: 498
; TYPE: PRT
; CRGANISM: Aspergillus Oryzae
US-10-820-200-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Aspergillus oryzae US-10-877-849-30
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US-10-815-495-18
                                                                                                      Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                             161 SSQDYFH 167
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100.0%; Score 40; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-10-228-063-45
i Sequence 45. Application US/10228063
i Sequence 45. Application US/10228063
i Publication No. US2003013585A1
i GENERAL INFORMATION:
i APPLICANT: Lanahan, Mike
i TITLE OF INVENTION: Self-processing Plants and Plant Parts
ILIE REFERENCE: 109846.317
i CURRENT APPLICATION NUMBER: US/10/228,063
i CURRENT PILLING DATE: 2002-12-12
i NUMBER OF SEQ ID NOS: 60
i SOFTWARE: PASTESQ for Windows Version 4.0
i SEQ ID NO 45
i LENGTH: 1095
i TYPE: RRI
i ORGANISM: Aspergillus shirousami
US-10-228-063-45
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative · 0; Mismatches 0; Indels
## APPLICANT: Tkaqi, Shinobu
| APPLICANT: Allain, Eric
| APPLICANT: Allain, Eric
| APPLICANT: Hjort, Carsten
| APPLICANT: Vikso-Nielsen, Anders
| TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
| FILE REFERENCE: 10490.500-US
| CURRENT APPLICATION NOWBER: US/10/877,849
| CURRENT APPLICATION NOWBER: US/10/877,849
| CURRENT FILING DATE: 2004-06-25
| NUMBER OF SEQ ID NOS: 43
| SEQ ID NO 36
| LENGTH: 640
| TYPE: PRT
| ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 7, 2005, 18:45:04 Job time: 4.7973 secs
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OTHER INFORMATION: Artificial
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November 7, 2005, 18:58:55; Search time 4.02703 Seconds (without alignments) 672.288 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                               2105692 seqs, 386760381 residues
                                                                                                                                                                                US-10-820-200-2_COPY_161_167
                                                                       OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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1 SSQDYFH 7
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                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                                                  Title:
Perfect
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geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_16Dec04:\* L:\_geneseqp1980s:\* geneseqp1980s:\* geneseqp20048:\* Database :

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abb09072 Aspergill	Aar46065 Mutant al	Aar72450 Aspergill	Aar78270 Aspergill	Aar79025 Mature ta	Aaw14500 Aspergill	Aab84206 Amino aci	Adt89632 Aspergill	Adt89628 Aspergill	Abp96630 Alpha-amy	н	ß	Aar88212 Alpha-amy	Aam24481 Human EST	Aao08447 Human pol	Aao02433 Human pol	Abb15756 Human ner	Adk47501 Streptoco	0	Abb71558 Drosophil	Aag64127 Human TNF	Adr95807 Novel S.	Aay90470 Yeast Sml	Aau31764 Novel hum	Aac08298 Human pol
ID.	ABB09072	AAR46065	AAR72450	AAR78270	AAR79025	AAW14500	AAB84206	ADT89632	ADT89628	ABP96630	ABP28341	AD061605	AAR88212	AAM24481	AA008447	AAO02433	ABB15756	ADK47501	ABB08450	ABB71558	AAG64127	ADR95807	AAY90470	AAU31764	AA008298
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Result No.	1	7	٣	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

128 5 ABB98330 131 4 AAO03876 134 7 AD032876 154 2 AAX30848 180 6 ABW92084 185 5 ABP26186 189 6 ABP76858 189 6 ABP76858 222 4 AAU31897 222 4 AAU31897 222 4 AAU3187 223 AAG33176 224 3 AAG33176 226 3 AAG33175 236 6 ABP96660 303 6 AD43877 303 6 AD43877 303 6 AD438877 317 7 AD0595026 318 6 ABP96616		Adk52505 Penicilli Aay30848 Human sec Abu00681 S. pneumo	တတ္သ	ZZ	Novel Zea ma	Aag33175 Zea mays Aag33174 Zea mays	Abul6660 Protein e Ada33877 Acinetoba	Adc95026 E. faeciu Abp98616 Mature Br	Aab96495 Putative
	ABB98330 AAO03876 ADD19267	ADK52505 AAY30848 ABU00681	ADM92084 ABP26186 ABP76858	ABP78080 AAU31887	ADQ66002 AAG33176	AAG33175 AAG33174	ABU16660 ADA33877	ADC95026 ABP98616	AAB96495
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Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation; protein co-ordinate data; 3 dimensional structure. Aspergillus oryzae TAKA protein (TAA). ABB09072 standard; protein; 423 AA. 99KR-00039130 99KR-00039130 (SAMY-) SAMYANG GENEX CORP. (first entry) (POST-) POSTECH FOUND WPI; 2001-534477/59. Aspergillus oryzae. Park GH; KR2001027418-A. 26-JUN-2002 09-SEP-1999; 09-SEP-1999; 06-APR-2001. ABB09072; Kim TJ, RESULT 1 ABB09072 

Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.

Disclosure; Page 188; 196pp; Korean.

3.2.1.133) having improved transmistance of matching arguments and any analysis having improved transmission activity, comprising using crystallisation and the three dimensional structure of maltogenic amylase comprises the following steps: (i) obtaining a gene of maltogenic amylase from Thermus sp. 1M6501 (KCTC 5027BP) and inserting the gene into plasmid pUC119 to construct recombinant DNA (pThMA119); (ii) inserting the recombinant DNA to Bscherichia coli MC1061, which is cultivated at 37 plus degrees Celsius for 10 hours in Luxia-Bertani (LB) media and centrifuging the media to obtain a microbial cell; (iii) suspending the microbial cell with buffer supernatant through column chromatography and obtaining purified maltogenic amylase is a dimer comprised of two The present invention describes manufacturing maltogenic amylase (BC

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AAR72450;
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maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase (TMAA) crystal. The amylase has a structure contenting an activated region that consists of amino acid residues of Asp-338, Glu-357, Asp-424, and a pocket with glucose bound that consists of amino acid residues of Pro44, TY145, Arg91, Arg91, Bro118, Cys116, Asn131, Glu1332, Va11329, and His1360. The present sequence represents Aspergillus oryzae TAKA protein (TAA), given in comparison with ThMA in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence os that of the Asoergillus oryzae alpha amylase, sold commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amylase exhibits a better activity level and better stability in the presence of oxidising agents than previous mutant alpha amylases, and improved thermostability at moderately low ph. The enzyme can be used as an additive for detergents, dishwashing agents and liquifaction agents. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant alpha-amylase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for use in detergents, dishwashing agents and liquefaction agents.
                                                                                                                                       Gaps
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                                                                                                                 DB 4; Length 423;
1.9;
                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                              Methionine substitution; stability; activity; detergent;
                                                                                                                                       Mismatches
                                                                                                                Score 7;
Pred. No.
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                                                                                                                 100.0%;
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                          Mutant alpha-amylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 478 AA;
                                                                                          Sequence 423 AA
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15-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                      Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modifications to improve washing and/or dishwashing performance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus derived alpha-amylase variants - having amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 2; Length 478; 100.0%; Pred. No. 2.1; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                      Aspergillus oryzae alpha amylase (mature protein).
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                                                                                                                          AAR72450 standard; protein; 478 AA.
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141 SSODYFH 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                      thermostable
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01-DEC-1995
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roft AH,

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13. .45
/label= loop 1 modification region
/label= loop 1 modification acid residue of a parent alpha
-anylase (used as a template for a variant) corresponding
to 7-23 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= loop 1 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
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residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 8-18 of AAW14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                           This sequence represents the mature form of taka-amylase from A. oryzae. This sequence was used in a method for the generation of mutant pullulanases for use in the food industry (see also AAR79026-28). The wild type pullulanase enzyme was modified by the method of the invention for enhancing the hydrophobicity of a selected site of the pullulanase. The method comprises replacement of a group in the selected site with a hydrophobic group, replacement of an amino acid with a hydrophobic amino acid, and/or insertion or deletion of a hydrophobic amino acid, and or deletion of a hydrophobic amino acid, selected site. The method was used to produce neopullulanases Y377F,
                                                                                                                                                                              Modifying a transferase by enhancing hydrophobicity of a selected site increases transfer activity, also new mutant neo-pullulanase(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl; Aspergillus oryzae; Bacillus amyloliquefaciens; altered property; calcium dependency; substrate binding; stability; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction; sweetener; ethanol production; variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4. .40
|abel= loop 1 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus oryzae alpha-amylase (mature protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 7; DB 100.0%; Pred. No. 2.1 iive 0; Mismatches
                                                                                                                                                                                                                                            Disclosure, Page 10-11, 18pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment; claim 35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW14500 standard; protein; 478 AA.
94JP-00288658
                                        93JP-00306096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
                                                                              (NIDE ) NEC CORP.
(EZAK ) EZAKI GLICO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 SSQDYFH 147
                                                                                                                                      WPI; 1995-279919/37.
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Misc-difference 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SSQDYFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S422V and M375L
                                        12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW14500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW14500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidation stable alpha amylases can be used for the simultaneous desizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or App. The parent alpha amylase is pref. derived from a Bacillus species, although alpha amylases of fungal origin can also be used. This sequence is the wild type (unmodified) alpha amylase of Aspergillus oryzae
          Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch; thermostable; methionine; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                simultaneous desizing and or starch derivs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild type; neopullulanase; B. stearothermophilus; mutant; food industry; modification; hydrophobicity; replacement insertion; deletion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                Nilsson TE
                                                                                                                                                                                                                                                                                                                                                                                                                                              oxidation stable alpha-amylase - for or scouring of fabrics contg. starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 25-26; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                Pedersen HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR79025 standard; protein; 478 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                            94WO-DK000371
                                                                                                                                                                                                                                                                                    94DK-00000141
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150. .164
240. .283
439. .474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mature taka-amylase A.
                                                                                                                                                                                                                                                                                                                                                                  Marcher D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 SSQDYFH 147
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-283767/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae.
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                                                                                                                      Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP07177891-A.
                                                                                                                                                            W09521247-A1
                                                                                                                                                                                                                                            05-OCT-1994;
                                                                                                                                                                                                                                                                                  02-FEB-1994;
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                                                                                                                                                                                                    10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUL-1995
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AAR79025

RESULT 5 AAR7902

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-amylase variants and methods of production - have altered properties such as calcium dependency, substrate binding and stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 maltose;
a variant) corresponding to 325-345 of AAW14498 is deleted or replaced with a fragment corresponding t fragment; claim 38"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltalcohol; starch; dough improver; brewing; starch liquification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sweeteners and ethanol from starch. See also AAW14498-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a fungamyl-like alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                              Borchert TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pedersen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 7; DB 2, 100.0%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 87-88; 171pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB84206 standard; protein; 498 AA
                                                                                                                                                                                                                                                                                                                                                                            Svendsen A, Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bisgard-Frantzen H, Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                   95DK-00000128.
95DK-00001192.
95DK-00001256.
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                                                                                                                                                                                        96WO-DK000057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 SSQDYFH 147
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-371424/37.
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tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSODYFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200134784-A1
                                                                                                                                                                                        05-FEB-1996;
                                                                                                                                                                                                                                   03-FEB-1995;
23-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-1999;
                                                                                               WO9623874-A1
                                                                                                                                                                                                                                                                                 10-NOV-1995
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                                                                                                                                             08-AUG-1996
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                                                                                                                                                                                                                              /label= loop 2 modification region
/note= "at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 44-57 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha-
amylase (used as template for a variant) corresponding
to 117-185 of AAW14499 is deleted or replaced with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-199 of AAW14499; claim 42"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -amylase (used as a template for a variant) corresponding to 195-202 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 21" 16. 173 modification region //note= "preferred region where at least one amino acid residue of a parent alpha amylase (used as a template for a variant) corresponding to 196-198 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                               /label= loop 1 modification region
/label= loop 1 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 14-15 of AAW14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 121-181 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291. 313
/label= loop 8 modification region
/label= loop 8 modification region
/note= "at least one amino acid residue of a parent alpha
-amilase (used as a template for a variant) corresponding
to 322-346 of AAW14498 is deleted or replaced with a
fragment corresponding to this fragment; claim 36"
                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "at least one amino acid residue of a parent alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-206 of AAW14499; claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= loop 8 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "at least one amino acid residue of a parent alpha
                                                                                                                                                                                                                                                                                                                                                                                            /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 48-51 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "an amino acid fragment corresponding to this region is deleted from the parent sequence of a variant Fungamyl; claim 43"
                          fragment corresponding to this fragment; claim 30"
  to 12-19 of AAW14499 is deleted or replaced with
                                                                                                                                                                                                                                                                                                                                                                         'label= loop 2 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102. .206
/label= loop 3 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= loop 3 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment; claim 26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment; claim 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment; claim 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181. .184
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                                               Misc-difference
                                                                                                                                                                                                           Misc-difference
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The present sequence represents a fungamyl-like alpha-amylase. The specification describes variants of this fungamyl-like alpha-amylase, which have an alteration in one the amino acid regions 90-110, 150-160, 161-167, 280-280, 448-455, and 468-475. Each alteration is a deletion or substitution of an amino acid or an insertion of an amino acid downstream of a particular position. The variants retain alpha-amylase activity, and have better heat stability and/or stability at acidic pH, relative to wild-type enzyme. The variants can therefore be used at higher reduced need for cooling and reduced risk of contamination). The variants may also be used in conjunction with other enzymes, particularly of high maltose content, or alcohol, from starch; as syrups, particularly of high maltose content, or alcohol, from starch; as dough improved for bled goods; in brewing, to increase fermentability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
                                             New variant of Fungamyl-like alpha-amylase, useful for production of malcose syrups, includes mutations that improve stability against heat and acidic pH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 7; DB 4; Length 498; 100.0%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus niger neutral alpha-amylase A (amyA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          the wort; and for liquefaction of starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADT89632 standard; protein; 498 AA.
                                                                                                                         Claim 1; Page 42-45; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVO ) NOVOZYMES BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2003; 2003US-0459902P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2004; 2004US-00815495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brody H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 SSQDYFH 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-708545/69.
               WPI; 2001-367478/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SSQDYFH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus niger.
                              N-PSDB; AAF90208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB, ADT89631
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004191864-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Connelly M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADT89632;
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Example 11; SEQ ID NO 22; 58pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance of glucoamylase (glad) and recovering heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase B (amyB) protein.
The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide sequences comprising modification of glucoamylase (glax) and recovering heterologous biological substance. Its present sequence is the
                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                  Length 498,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus niger neutral alpha-amylase B (amyB) protein.
                                                                                                                   Aspergillus niger neutral alpha-amylase A (amyA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glucoamylase; glaA; amyB; alpha-amylase B; enzyme
                                                                                                                                                                                  100.0%; Score 7; DB 8; 100.0%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 7; DB 8; 100.0%; Pred. No. 2.2;
                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2003; 2003US-0459902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-2004 (first entry)
                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                             162 SSQDYFH 168
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                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Connelly M, Brody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus niger.
                                                                                                                                                                                                                                                      1 SSQDYFH
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                                                                                                                                                      Sequence 498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004191864-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substance
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Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, antiinflammatory, infection, vaccine, meningitis, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                        Streptococcus polypeptide SEQ ID NO 5858
                         ABP28341 standard; protein; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-2001; 2001WO-GB004789.
                                                                                                              02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                           Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-352536/38.
N-PSDB; ABN68972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                  WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Telford J,
Tettelin H;
                                                                     ABP28341;
                           The present invention describes polynucleotides which encode processing enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose isomerase, or glucoamylase) that are optimised for expression in plants. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic processing enzymes, which are activated under suitable conditions to act upon the desired substrate. Also described are self-processing transgenic plants and plant parts, e.g. grain, which express one or more of these enzymes and have an altered composition that facilitates plant and grain processing. Also described is a method (M) for converting starch to starch-derived products in a transformed plant part (TPP), by activating the starch processing enzyme contained in it. Transgenic grain is useful or produce food products having improved taste and to produce fermentable substrates for ethanol and fermented beverages. (M) eliminates the need to mill or physically disrupt the integrity of plant parts prior to recovery of starch-derived products. The present sequence represents alpha-amylase/glucoamylase fusion protein, which is given in the example integrity of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide encoding hyperthermophilic processing enzymes e.g. alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.
                                                                                                                                                                                                                                                                                       Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch; maltodextrin; ethanol; fermentation; beverage; enzyme.
                                                                                                                                                                                                                                               Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinkema M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 7; DB 6; Length 1095; 100.0%; Pred. No. 4.2; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Batie CJ, Chen W,
                                                                                                            ABP96630 standard; protein; 1095 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2002; 2002WO-US027129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2001; 2001US-0315281P.
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus shirousami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Basu SS,
162 SSQDYFH 168
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N-PSDB; ACC44572.
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                                                                                                                                                                                                   02-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                        ABP96630;
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Masignani V, Margarit Y RosI, Grandi G, Fraser C;

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS) gequences (S1), given in the specification. The proteins have antibacterial and antinflammatory the specification. The proteins have antibacterial and antinflammatory activity. (1), nucleic acids encoding (1), ABM6044-ABN71256 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Nucleic acids encoding (1) are used to detect Streptococcus in a streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to detect Streptococcus in a composition comprising (1) or a nucleic acid encoding (1), may be consed as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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0
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 14; ive 0; Mismatches
Claim 1; Page 3748; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO61605 standard; protein; 351 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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ID ADO6
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Gaps

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Best Local Similarity 100. Matches 7; Conservative

Gaps

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Claim 16; SEQ ID NO 72; 510pp; English
                 Transcription factor G319, SEQ ID 72.
                                                                                                   (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                  18-SEP-2002; 2002US-0411837P.
                                                                                       17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                         18-SEP-2003; 2003WO-US030292
        15-JUL-2004 (first entry)
                                                                                                             Jiang C, Heard JE,
Riechmann JL, Haake
                                               Arabidopsis thaliana
                                                                                                                          WPI; 2004-330163/30.
N-PSDB; ADO61604.
                                                       WO2004031349-A2.
                                                                 15-APR-2004.
ADO61605;
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A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS 224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562) stoolated from a T. lanuginosus gene library. The recombinant enzyme (54-60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7 and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermophilic alpha-amylase with activity range of 60-80 degrees C - derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
                                                                                                Length 351;
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                                                                                                                                                  0; Indels
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100.0%; Pred. No. 33;
iive 0; Mismatches
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8
                                                                                                85.7%; Score 6; DB 8 100.0%; Pred. No. 25; ive 0; Mismatches
ftp.wipo.int/pub/published_pct_sequences.
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/label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                AAR88212 standard; protein; 493 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                      Query Match
Best Local Similarity luv.
6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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                                                                                                                                                                                                                                              226 SSQDYF 231
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                                                  Sequence 351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 493 AA;
                                                                                                                                                                                                1 SSODYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-amylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9601323-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                  AAR88212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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AAM24481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel plant transcription factor proteins (1) and nucleotide sequences (II) (ADD61534-AD063779). The proteins (I) and nucleotide sequences (II) (ADD61534-AD063779). The proteins (II) and nucleotide sequences (III) (ADD61534-AD063779). The sequences can be used to produce transgenic plant compared to a non-transgenic plant compared to an altered trait selected from increased tolerance to abiotic stress, increased tolerance to council in cold, increased tolerance to conditions, increased tolerance to cold, increased tolerance to low nitrogen conditions, increased tolerance to low nitrogen sensing, increased tolerance to low nitrogen conditions, increased tolerance to low nitrogen sensing, increased tolerance to seased tolerance to multiple fungal pathogens, increased testance to conditions, increased testance to conditions, increased testance to conditions, increased testance to suggers, altered carbon/nitrogen sensing, early flowering, latered carbon/nitrogen sensing, early flowering, altered flower structure, loss of thower determinacy altered sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity and altered flower structure, loss of thower determinacy altered send morphology, altered vascular tissue structure, reduced altered stem morphology, altered vascular tissue structure, reduced altered stem morphology, altered vascular tissue structure, reduced altered stem morphology, altered vascular tissue structure, reduced altered trichome structure, altered seed development, altered coll flower structure, altered seed development, altered seed development, altered coll proliferation, altered seed development, altered seed colloration, altered seed distance, altered seed development, altered seed ordoration, altered seed ordoration, altered seed colloration, altered seed ordoration, altered seed ordoration, altered seed ordorat
                                                                                                                                           Plant; transcription factor; transgenic plant; abiotic stress tolerance; semotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low hosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reuber TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adam LJ, Re
Sherman BK;
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Gaps

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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 22339; 1399pp + Sequence Listing; English
                                                                                26-FEB-2001; 2001WO-US004927.
                                                                                                                                                             Tang YT, Liu C, Drmanac RT,
                                                                                                    28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                     WPI; 2001-514838/56.
                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                N-PSDB; AAI88378
                                   WO200164835-A2
              Homo sapiens.
                                                          07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                      Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomator. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                                                         Chen R, Asundi V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                       YT, Liu C, Zhou P, Qian XB, Wang Z,
?, Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.4%; Score 5; DB 4
100.0%; Pred. No. 70;
iive 0; Mismatches
                                                                   Human EST encoded protein SEQ ID NO: 2006.
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page 1269; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA008447 standard; protein; 52 AA
AAM24481 standard; protein; 45
                                                                                                                                                                                                                                         25-JAN-2000; 2000US-00491404.
17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00663870.
                                                                                                                                                                                                                     25-JAN-2001; 2001WO-US002687
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100...
Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein of the invention
                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-476164/51.
N-PSDB; AAH99140.
                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 SQDYF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SQDYF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45 AA;
                                                                                                                                                                        WO200154477-A2
                                                                                                                                                   Homo sapiens.
                                             12-0CT-2001
                                                                                                                                                                                              02-AUG-2001
                       AAM24481,
                                                                                                                                                                                                                                                                                                                       Tang YT,
Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
AAO08447
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.

Human polypeptide SEQ ID NO 22339.

(first entry)

06-NOV-2001

AAO08447;

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of canoer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 5; DB 4; Length 52; 100.0%; Pred. No. 79; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7, 2005, 19:27:58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: November
Job time: 7.02703 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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7, 2005, 19:15:40; Search time 0.851351 Seconds (without alignments) 791.116 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                           November
                                                                                                                                                           Run on:
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US-10-820-200-2\_COPY\_161\_167 OLIGO Gapop 60.0 , Gapext 60.0 1 SSQDYFH 7 Title: Perfect score: Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

0

Word size :

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. S	Score	Query Match	% Query Match Length	Α !	SUMMARIES	[ption
	ر د	100.0	478 498	0 0	JK0201 A48305	
	r 1	100.0	499	Н-	ALASI	alpha-amylase (EC
	, ,	100.0	499	1 (2)	JS0663	. o
	7	100.0	499	N	JT0466	0)
	7	100.0	499	N	JN0588	a)
	7	100.0	499	~	B48305	8
	7	100.0	624	Н	JC4510	pullulanase (EC 3.
	9	85.7	317	7	E84088	restriction endonu
	ø	85.7	351	~	E86187	.⊢
	Ŋ	71.4	104	~	S49803	
	5	71.4	129	~	H71046	hypothetical prote
	ហ	71.4	144	~	JC7121	_
	'n	71.4	178	~	H96905	hypothetical prote
	S	71.4	180	~	B95039	hypothetical prote
	ß	71.4	217	Н	S61191	ical h
	ហ	71.4	253	N	A05283	
	2	71.4	289	N	A43562	
	2	71.4	295	~	B84747	
	2	71.4	326	~	AF2082	
	'n	71.4	330	N	H75068	
	2	71.4	330	~	B71163	ligop
	Ŋ	71.4	331	~	T06227	peroxidase (EC 1.1
	'n	71.4	332	7	T10790	peroxidase (EC 1.1
	ហ	71.4	420	~	T42616	envelope protein -
	Ŋ	71.4	423	~	A12189	hypothetical prote
	ហ	71.4	426	~	H71483	
	2	71.4	459	7	H81324	

141 SSODYFH 147

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7

1 SSQDYFH

Librar amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Accession: A48305
R;Korman, D.R.; Bayllss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe A;Reference number: A48305; MUID:90254827; PMID:2340591

A,Accession: A48305
A,Status: preliminary; not compared with conceptual translation A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-498 < KOR>
A,Cross-references: UNIPROT: Q02905
C,Function:

ö

## ALIGNMENTS

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A; Cross-references: UNIPROT:P10529
A; Cross-references: UNIPROT:P10529
C; Comment: One atom of calcium per molecule is essential for the activity.
C; Comment: This enzyme is a glycoprotein.
C; Comment: See also PIR:JT066 and PIR:JS0240.
C; Comment: See also PIR:JT066 and PIR:JS0240.
C; Punction:
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Pathway: glycogen/starch degradation C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation F;173-300/Domain: alpha-amylase core homology <AMY.
F;197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;210,230,297/Active site: His, Glu, Asp #status experimental
alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae
N;Alternate names: glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31.Mar.1991 #sequence_revision 31.Mar-1991 #text_change 09-Jul-2004
C;Accession: JK0201
R;Toda, H; Kondo, K; Narita, K.
R;Toda, H; Kondo, K; Narita, K.
A;Title: The complete amino acid sequence of Taka-amylase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                  A;Reference number: JK0201
A;Accession: JK0201
                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein A;Residues: 1-478 <TOD>
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Length 499
                                                                                                                                                                                                                                                                                                                                  100.0%; Score 7; DB 1;
100.0%; Pred. No. 0.35;
ive 0; Mismatches
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Pred. No. 0.35;
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                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SSQDYFH 7
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A; Residues: 1-499 <WIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-499 <WI2>
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Advantage (EG. 72.11); precursor (validated) - Aspergillus oryzae

Advantage (EG. 72.11); precursor (validated) - Aspergillus oryzae

C. Secise - Aspergillus oryzae, ase kocyme 112 glycogenses Fraka smylase A

C. Accession: Sofista Anizity in Midhardt, G.; Rutckowski, E.

A. Arttesi, S.; Lachmund, A.; Wildhardt, G.; Rutckowski, E.

A. Arttesi, S.; Lachmund, A.; Wildhardt, G.; Rutckowski, E.

A. Arttesi, S.; Lachmund, A.; Wildhardt, G.; Rutckowski, E.

A. Arttesi, S.; Lachmund, A.; Wildhardt, G.; Rutckowski, E.

A. Arttesi, S.; Lachmund, A.; Wildhardt, G.; Rutckowski, E.

A. Arcession: Sofista Anizity (Sociation Program of Anizity) PIDN: CAN31218.1; PID: 2295921

A. Arcession: Sofista Anizity (Sociation Program of Anizity) PIDN: CAN31218.1; PID: 2295921

A. Arcessides L. Type (MIR)

A. Arcessides L. Argo (MIR)

A. Arcession: A. A. Appreciation (Anizity)

A. Arcessides L. Appreciation (Anizity)

A. Arcessides L. Appreciation (Anizity)

A. Arcessides L. Appreciation (Anizity)

A. Arcession: A. A. Arcession: Anizity

A. Arcession: A. A. Arcession: A. Arcession (Anizity)

A. Arcession: A. Arcession: A. Arcession (Anizity)

A. Arcession: 
catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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                         A:Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Reywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                     Length 498;
                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                  DB 2;
0.35;
                                                                                                                                                                ; Score 7; DB 2; Pred. No. 0.35
0; Mismatches
                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative 0
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  A; Description:
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A,Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keyvords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; poly.
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase 1 #status experimental <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;1-5,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Aan) (Guvalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
A;Accession: A33215
A;Status: translation not shown
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R; Genes, M.J; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A; Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing, A; Reference number: JS0240; MUID:89378767; PMID:2789162
A; Residues: 1-499 cGEN>
A; Residues: 1-499 cGEN>
A; Residues: 1-499 cGEN>
A; Residues: JS0240; M.; Kakudo, M.
A; Rusunoki, M.; Harada, W.; Kakudo, M.
J. Blochem. 95, 697-702, 1984
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(S. Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

(S. Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

(S. Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

F;1-21/Domain: alpha-amylase 3 # status predicted <51G>
F;22-499/Product: alpha-amylase 3 # status experimental <AMY>

F;194-3121/Domain: alpha-amylase core homology <AMY>
F;51-59,171-185,261-304,461-496/Disulfide bonds: # status experimental

F;192,181-181,181-181 site: calclum (Asn, Glu, Asp, His) # status predicted

F;218/Binding site: carbohydrate (Asn) (covalent) # status experimental

F;218/Binding site: carbohydrate (Asn) (covalent) # status experimental
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NyAlternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C;Species Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S04549; A33215; A44713
R;Wirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon A;Reference number: S04548; MUID:89237897; PMID:2785629
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A;Contents: annotation; X-ray crystallography, 3.0 angstroms
C;Comment: One atom of calcium per molecule is essential for activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Title: Structure and possible catalytic residues of Taka-amylase A.
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A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 499
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alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
NyAlternate names: Taka-amylase A
NyAlternate names: Taka-amylase A
NyAlternate names: Taka-amylase A
C;Specias: Aspergillus oryzae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JN0588
R;Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kirita, N.; Tsuboi, A.; Udaka, S.
Gene 84, 319-327, 1989
A;Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for m
A;Reference number: JN0588; MUID:90128276; PMID:2612911
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C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession. B48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe
A;Reference number: A48305; MUID:90254827; PMID:2340591
A;Accession: B48305
A;Status: preliminary; not compared with conceptual translation
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A, Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C, Superfamily: Aspergillus alpha-amylase; plyropacein; glycosidase; hydrolase; polysaccharide degradation
F,194-321/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <MT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Comment: The alpha amylases are encoded by multigene family.
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100.0%; Pred. No. 0.35;
tive 0; Mismatches (
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C; Function:
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Matches 7; Conservative
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Best Local Similarity
Matches 7: Conserv
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A,Molecule type: mRNA
A,Residues: 1-499 <TSU>
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Cibate: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
Cibate: 17-Aug-1992 #sequence_revision 17-Aug-1999
Cibate: 17-Aug-1992 #sequence_revision 17: Hara, S.
Biost: Biotechnol. Biochem. 56, 174-179, 1992
A; Title: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expression A; Reference number: 150663; MUD:92323146; PMID:1368777
A; Accession: J50663
A; MuD:9223146; PMID:1368777
A; Residuce rumber: J50663
A; MuD:9223146; PMID:1368777
A; Residuce: 1-499 cSHI>
C; Function:
A; Pesthwas: 1-499 cSHI>
C; Function: A; Pathway: glycogen/starch degradation C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: glycoprotein; glycosidase; hydroilase; polysaccharide degradation C; Keywords: glycoprotein; glycosidase; hydroilase; polysaccharide degradation F; 12-499/Product: alpha-amylase #status predicted cALb>
F; 18/10omain: alpha-amylase core homology cAMY>
F; 18/10omain: alpha-amylase core homology cAMY>
F; 18/10omain: alpha-amylase core homology cAMY>
F; 18/10omain: alpha-amylase (Asn) (covalent) #status predicted
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R;Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A;Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergill
A;Reference number: JT0466
A;Rolecule type: DNA
A;Residues: 1-499 <TAD>
A;Cromment: See also PTR:JK0201 and PTR:JS0240.
C;Comment: See also PTR:JK0201 and PTR:JS0240.
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics:
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Comment: signal sequence #status predicted <AMT>
C;FL1/Domain: signal sequence #status predicted <AMT>
C;Comment: Appleance #status predicted <AMT>
C;Comment: See also PTR:JK0201 and PTR:JK0201 and JY0301 and JY
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Species: Aspergillus oryzae
Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
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194-321/Domain: alpha-amylase core homology <AMY>
218/Binding site: carbohydrate (Asn) (covalent) #status predicted
;231,251,318/Active site: His, Glu, Asp #status predicted
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        Indels
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Best Local Similarity 100.
Matches 7; Conservative
7; Conservative
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Best Local Similarity
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CiAccession: E86187

RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Tankins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: E86187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT:023041; GB:AE005172; NID:g2388568; PIDN:AAB71449.1; GSPDB:GR
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C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: H71046
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir.
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchn
DNA Res. S, 55-76, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pypothetical protein YML058w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YM9958.04
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: $49803
R;Devlin, K.; Churcher, C.
R;Devlin, K.; Churcher, C.
A;Reference number: $49800
A;Reference number: $49800
                      YUP8H12.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Pred. No. 22;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%; Score 6; DB 2
100.0%; Pred. No. 4;
Live 0; Mismatches
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A;Map position: 13L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.C
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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A; Residues: 1-104 <DEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-351 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
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UNALIZATE DAMES (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)

NALerrate names : Lixth protein; raw starch-degrading amylase
Ny.Alerrate names : Lixth protein; raw starch-degrading amylase
Ny.Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C.Species: Lipomyces kononenkoae: dealpha-glucosidase (EC 3.2.1.41)
C.Species: Lipomyces kononenkoae: dealpha-glucosidase (EC 3.2.1.41)
C.Species: Lipomyces kononenkoae: voision 21-Aug-1996 #text_change 09-Jul-2004
C.Accession: UG4510; PC4116
R.Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A.Title: Clohing; sequence analysis and expression in yeasts of a cDNA containing a Lipomyces on the containing a Lipomyces and the containing both alpha-1,4 and alpha-1,6 linkages hydomin: signal sequence #status predicted *AiGone: Lixth C.Function:
A.Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages A.Pentition: hydrolyzes alpha-amylase; alpha-amylase core homology second starch degradation of Superfamily: Lipomyces alpha-amylase status predicted *AiGone: Lixth C.Function:
A.Description: signal sequence #status predicted *AiGone: Lixth C.Function:
A.Description: signal sequence #status predicted *AiGone: P. 29-64 Product: alpha-amylase starch-binding domain homology *AMY.
F.29-64 Product: alpha-amylase starch-binding domain homology *AMY.
F.29-64 Production: alpha-amylase starch-binding domain homology *AMY.
F.20-64 Production: alpha-amylase starch-binding domain homology *AMY.
F.20-64 Production: alpha-amylase starch-binding domain homology *AMY.
F.177-185, 299-71 Alphanding site: His, Glucyalending predicted
F.1357,377,444 Akactive site: His, Glucyalending predicted
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Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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Best Local S:
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Search completed: November 7, 2005, 19:33:48 Job time: 1.85135 secs
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C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Date: 10-Sep-2001 #sequence_revision #seton.
C;Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Batteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A9690; MuID:21359325; PMID:21359325
A;Accession: H9605
A;Residues: L-178 «KUR>
A;Molecule type: DNA
A;Residues: 1-178 «KUR>
A;Coss-references: UNIPROT:097MZ1; GB:AE001437; PIDN:AAK78035.1; PID:g15022870; GSPDB:G
A;Genetics:
A;
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C;Species: Armadillidium vulgare (common pill bug)
C;Species: Armadillidium vulgare (common pill bug)
C;Accession: JC7121
B;Okuno, A; Hasegawa, Y; Ohira, T; Katakura, Y; Nagasawa, H.
B;Okuno, A; Hasegawa, Y; Ohira, T; Katakura, Y; Nagasawa, H.
B;Okuno, A; Hasegawa, Y; Ohira, T; Katakura, Y; Nagasawa, H.
B;Okuno, A; Hasegawa, Y; Ohira, T; Katakura, S; Nagasawa, H.
B;Okuno, A; Hasegawa, Y; Ohira, T; Katakura, S; NID:10529379
A;Title: Characterization and cDNA cloning of androgenic gland hormone of the terrestria A;Reference number: JC7121; MUD:20001935; PMID:10529379
A;Accession: JC7121
A
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A1000; MUID:98344137; PMID:9679194
A;Accession: H71046
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-129 «KMA>
A;Residues: 1-129 «KMA>
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Gene: Phis accession replaces an interim accession for a sequence replaced by GenBank
A;Gene: PH1664
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100.0%; Pred. No. 29;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
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7, 2005, 19:00:20 ; Search time 3.71622 Seconds (without alignments) 964.571 Million cell updates/sec
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Compugen Ltd.
  GenCore version
Copyright (c) 1993 - 2005
                                                                                  OM protein - protein search, using sw model
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US-10-820-200-2\_COPY\_161\_167 Perfect score:

1 SSQDYFH 7 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

1612378 seqs, 512079187 residues Searched:

0 Word Bize : 1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description				Q02906 aspergillus								Q8e4p7 streptococc	_			-				•	Q677el hyacinthus		-			Q9u8r2 armadillidi	Q9cuq8 mus musculu	Q73gi6 treponema d		-	Q97sk2 streptococc
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0	Q70bc3 pseudomonas Q70bc3 volinella s Q7ysz6 rhodnius pr Q8eut6 mycoplasma
0611G1 08E118 TDX TRYBR TDX TRYB Q71EY2 Q71SQ4 Q9U4F2 P97975 HNT2 YEAST Q9CUH9	Q70BE3 Q7M8C0 Q7YSZ6 Q8EUT6
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## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                 Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
"Cloning, characterization, and expression of two alpha-amylase genes
from Aspergillus niger var. awamori.";
Curr. Genet. 17:203-212(1990).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
-!- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolism; Glycoprotein; Glycosidase;
                                                                                                                                                                                       Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
                                                                    25-OCT--2004 (Rel. 34, Last sequence update)
Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan)
Alpha-amylase A).
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Nucleophile (By similarity).
Proton donor (By similarity).
By similarity.
Calcium 1 (By similarity).
                                 498 AA.
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InterPro; IRR006647; Alpha amyl_cat.
InterPro; IRR006047; Alpha amyl_cat.
InterPro; IRR006046; Glyco_hdro_l3.
Fam; PR00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM06642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism
Hydrolase; Multigene family; Signal.
                                 PRT;
                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
STRAIN=UVK143F;
MEDLINE=90254827; PubMed=2340591;
                                                                  (Rel. 34, Created)
(Rel. 34, Last seq
(Rel. 45, Last ann
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PIR; A48305; A48305.
HSSP; P10529; 7TAA.
                                 STANDARD:
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MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
TSUKAGOSHI N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Udaka S.;
"Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
evidence for multiple related genes.";
Gene 84:319-327(1989).
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
"Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
Aspergillus oryzae.";
Agric. Biol. Chem. 53:593-599(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [6] SEQUENCE OF 206-225.

SEQUENCE OF 206-225.

MEDLINE=74001521; Pubmed=4733850;

ISEMUTA S., Ikenaka T.;

"The amino acid sequences of glycopeptides obtained from Taka-amylase A with trypsin and chymotrypsin.";

J. Biochem. 74:1-10(1973).
                                                                                                                                                                                                                                                                        MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6; Genes M.J., Dove M.J., Seligy V.L.; "Aspergilus oryzae has two nearly identical Taka-amylase genes, each containing eight introns."; Gene 79:107-117(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
Brzozowski A.M., Davies G.J.;
Brzozowski A.M., Davies G.J.;
"Structure of the Aspergillus oryzae alpha-amylase complexed with the inhibitor acarbose at 2.0-A resolution.";
Blochemistry 36:10837-10845(1997).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-80227691; PubMed-6156152;
Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
Toda H., Narita K., Kakudo M.;
Toda H., Naritu K., Kakudo M.;
A. Fodeulur Furcture of taka-amylase A. I. Backbone chain folding at 3-A resolution.";
J. Biochem. 87:1555-1558(1980).
                                                     Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                      STRAIN=DSM 63303; PubMed=2785629; MEDLINE=9837897; PubMed=2785629; Wirsel S., Lachmund A., Wildhardt G., Ruttkowski E.; Wirsel S., Lachmund A., Mildhardt G., Ruttkowski E.; "Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-84212370; PubMed-6609921;
Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
"Structure and possible catalytic residues of Taka-amylase A.";
J. Biochem. 95:697-702(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 22-499.

Toda H., Kondo K., Narita K.;

"The complete amino acid sequence of Taka-amylase A.";

Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982)
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                                       Aspergillus oryzae.
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                                                                                     NCBI_TaxID=5062;
                       Name=AMY3;
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Aspergillus kawachi (Aspergillus awamori var. kawachi).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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            similarity).
Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (B similarity).
Calcium 2 (By similarity).
By similarity.
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P10529; P11763; Q002.0.
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
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Calcium 1 (via carbonyl oxygen)
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SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Q76CT3

RESULT 2 Q76CT3

Matches

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AWYA ASPOR 1D AWYA AS AC P10529-DT 01-0CT-DT 25-0CT-DE Alpha-1 GN Name=Al GN and GN and GN Ame=Al

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STRAIN=UVK143F;
MEDLINB=90254827; PubMed=2340591;
Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
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1-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase B).
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Q02906;
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AMYB_ASPAW
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                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensea agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         at high concentrations.

1- SUBUNIT: Monomer.

1- SUBUNIT: Monomer.

1- SUBUNIT: Monomer.

1- SIBUNIT: Monomer.

1- SIBUNITARITY: Belongs to the glycosyl hydrolase 13 family.
COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR006046; Alpha amyl cat.
InterPro; IPR006046; Glyco-hydro_13.
Pract Pro; IPR006046; Glyco-hydro_13.
Pro; PR00110; ALPHAAMYLASE.
SMART; SM00642; Aamy; 1.
3D-structure; Calcium-binding; Carbohydrate metabolism;
Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium 1 (via carbonyl oxygen).
Calcium 1.
Calcium 2.
Calcium 2.
Calcium 1 (via carbonyl oxygen).
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0 -> Y (in Ref. 5).

P -> L (in Ref. 3).

G -> V (in Ref. 3).

G -> V (in Ref. 3).

I -> L (in Ref. 4).

I -> L (in Ref. 5).

L -> A (in Ref. 5).

WPIY -> PYI (in Ref. 5).
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/FTId=CAR_000125.
Q -> R (in AMY3).
F -> L (in AMY3).
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-> S (in Ref. 5)
-> SD (in Ref. 5)
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Proton donor
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EMBL, X12726; CAA31219.1; --
EMBL, X12727, CAA31220.1; --
EMBL, D00434; BAA00336.1; --
EMBL, M33218; AAA32708.1; --
PIR; JT04066; JT0201.
PIR; JT04666; AT0466.
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M3218; AAA32708.1; PIR; JK0201; JK0201.
PIR; JK0201; JK0201.
PIR; JK0466; JK0466.
PIR; S04548; ALAS1.
PDB; ZTAA; X-ray; A=22-499.
PDB; JTAA; X-ray; @=22-499.
PDB; TTAA; X-ray; @=22-499.
PDB; TTAA; X-ray; @=22-499.
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Gaps

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DINE=92323146; PubMed=1368777;
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                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
HSSP, P10529; 77AA.
InterPro: IPR006589; Alp amyl_cat_sub.
InterPro: IPR006046; Alpa_amyl_cat.
InterPro: IPR006046; Glyco hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAWYLASE.
SMART; SM00642; Aamy; 1.
Hydrolase; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
VCBI_TaxID=5070;
[1]
                                                                                                                                                                                                                                                                                                  (By
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                                                                                                                                                                                                                                                                                                                                                                                          .) (Potential)
                                                                                                                                                                                                                                                                                                               Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (B similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
Noblemed (GlCNAC. . .) (Potential)
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By similarity.
By similarity (By similarity).
Calcium I (via carbonyl oxygen)
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2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan Name-AMY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                Nucleophile (By similarity)
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100.0%; Pred. No. 2.4
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                          similarity)
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218
499 AA;
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P30292;
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Matches
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AMY_ASPSH
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                                                                                                                                                                                                                                                                                                                                                                                           noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
Shibuya I., Tamura G., Ishikawa T., Hara S.;
"Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its
"Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its
expression in Saccharomyces cerevisiae.";
Biosci. Biotechnol. Biochem. 56:174-179(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
-!- COFACTOR: Binda 2 calcium ions per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
By similarity.
Whinked (GlCNAC. ..) (By similarity).
Whinked (GlCNAC. ..) (By similarity).
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Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Signal.
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TAXID=5062;
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Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-amylase.
Nucleophile (By similarity).
Proton donor (By similarity)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Taka-amylase A (EC 3.2.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   499 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR006589; Alp_amyl_cat_sul
InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_l3.
Pfam; PF00128; Alpha-amylase; I.
PRINTS; PR00110; ALPHAAMYLASE.
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59 By
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496 By
218 NV-
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Matches 7: Conser
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Fakhoury A.M., woloshuk C.P.;

"Amy1, the alpha-amylase gene of Aspergillus flavus: Involvement in a flatoxin biosynthesis in maize kernels.";

"Amy1, the alpha-amylase gene of Aspergillus flavus: Involvement in a flatoxin biosynthesis in maize kernels.";

"Phytopathology 89:908-914(1999).

"I SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

"EMB1, AF139925; AR18464.1, -..

"AF139925; AR18464.1, -..

"GO; GO:0004556; F:alpha-amylase activity, acting on glycosyl bonds; IEA.

"GO; GO:0005975; P:carbohydrate metabolism; IEA.

"R GO; GO:0005975; P:carbohydrate metabolism; IEA.

"R GO; GO:000649; Alpha-amylase; aub.

"InterPro: IPR006646; Glyco_hydro_13.

"R InterPro: IPR006646; Glyco_hydro_13.

"R PRINTS; PR00110; ALPHAAMYLASE.

"R SMART; SM00642; Aamy; 1.

"M Glycosidase; Mydrolase.

"M Glycosidase.

"M G G G G G G G G G G G 
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=IGC4052B; Pubmed=8529895; DOI=10.1016/0378-1119(95)00633-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steyn A.J.C., Marmur J., Pretorius I.S.; "Cloning, sequence analysis and expression in yeasts of a CDNA containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipomyces kononenkoae.
Eukaryota, Pungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Lipomycetaceae; Lipomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annocation update)
Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;
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Last annotation update)
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100.0%; Pred. No. 2.4;
ive 0; Mismatches
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                                                                                                                                                            499 AA
                                                                                                                                                                                                                             Created)
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MEDLINE=96132108; PubMed=8593683;
Steyn A.J.C., Pretorius I.S.;
                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Alpha-amylase (EC 3.2.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
Les 7; Conservative
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                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 166:65-71(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 SSQDYFH 168
162 SSQDYFH 168
                                                                                                                                                                                                                                                                                                                                                           Name=amyl;
Aspergillus flavus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SSQDYFH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=86-10D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMY1 LIPKO
Q01117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                            Q7LV45
Q7LV45;
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AMY1_LIPKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                               Discrete of the control of the contr
                                                                                                                                                         "Molecular cloning and characterization of a transcriptional activator gene, amyR, involved in the amylolytic gene expression in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=105351;
                                                                                           Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Matsubara T.;

Whatsubara T.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

L. SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

EMBLS, AB083159; BAD06002.1;

R. GO: GO:0004556; F:alpha-amylase activity; IEA.

R. GO: GO:0005975; P:carbohydrate metabolism; IEA.

R. InterPro; IPRO06047; Alpha-amyl.cat.

R. InterPro; IPRO06046; Glyco_hydro_I3.

R. InterPro; IPRO06046; Glyco_hydro_I3.

R. Pfam; PP00128; Alpha-amylase; I.

R. RHITS; PR00110; Alpha-amylase; I.

R. SWART; SM00642; Aamy; I.
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Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 7; DB 2; Length 499; 100.0%; Pred. No. 2.4; ... ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;
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2B357AE38B36C1C2 CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-amylase precursor.
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                                                                MEDLINE=20289310; PubMed=10830498;
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SEQUENCE 499 AA; 54794 MW;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 SSQDYFH 168
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SEQUENCE FROM N.A.
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                                                                                                                                 Limura Y.;
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Q76L99;
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Q76L99
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Gaps

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Length 499; 0; Indels

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"Cloning and expression of Lipomyces starkeyi alpha-amylase in Escherichia coli and determination of some of its properties."; FEMS Microbiol. Lett. 233:53-64(2004).
EMBL: AXLIS-6453; AAN/5021.1; --
HSSP; P26827; 1A47.
                                                          STRAIN=KSM 22M;
PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
Moon T.-W.;
                                                                                                                                                                                                                                  GO, GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IRR0066047; Alpha-amyl_cat.
InterPro; IRR006689; Alp amyl_cat_sub.
InterPro; IRR005036; CBM_21.
Pfam; PF00128; Alpha-amylase; 1.
Pfam; PF0370; CBM_21; 1.
SMART; SM0642; Aamy; 1.
SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
les 7; Conservative
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                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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SEQUENCE 183 AA;
    NCBI_TaxID=29829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; SAG1281; -.
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      OX REAL TO THE SERVICE OF THE SERVIC
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                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                "Characterization of a novel alpha-amylase from Lipomyces kononenkoae
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                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P10529; 7TAA.
InterPro; P18006099; Alp amyl cat sub.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR005036; CBM 21.
Pfam; PF001370; CBM 21; 1.
SMART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-amylase 1.

Garbobydrate binding type-21.

Nucleophile (By similarity).

Proton donor (By similarity).

By similarity.

Calcium 1 (By similarity).

Calcium 1 (via carbonyl oxygen) (By similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
Calcium 2 (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlcNAc. . . ) (Potential).
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Lipomyces starkeyi.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Lipomycetaceae; Lipomyces.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U30376; AAC49622.1; ALT_INIT.
PIR; JC4510; JC4510.
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Best Local Similarity luv...
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05-JUL-2004 (TrEMBLrel.
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344
344
624 AA;
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ACT_SITE
ACT_SITE
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CARBOHYD
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SEQUENCE
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STRAIN=2603 V/R / Serotype V;
STRAIN=2222988; Pubméd=1220547; DOI=10.1073/pnas.182380799;
MEDLINE=2222988; Pubméd=1220547; DOI=10.1073/pnas.182380799;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobhin E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
100.0%; Score 7; DB 2; Length 647; 100.0%; Pred. No. 3;
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                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 AA; 21278 MW; 029AD020DF762720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein SAG1281.
OrderedLocusNames=SAG1281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%; Score 6; DB 2;
100.0%; Pred. No. 14;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                183 AA
                     100.0%; Pred No. 100.0%; ive 0; Mismatches
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Gaps

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Indels

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Pred. No. 20;

Mismatches

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100.08; Pr.
                    Best Local Similarity 100.
Matches 6; Conservative
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STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=NRRL Y-1140;
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                                                                                                                           123 SSODYF 128
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Q9K764;
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Q6CUY2
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Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 35405 / DSM 14222;
STRAIN=ATCC 35405 / DSM 14222;
SUBMED=10.0073/pnas.0307639101;
PubMed=15064399; DOI=10.1073/pnas.0307639101;
Seshadiri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F., Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H., Selngut J., Ren Q., Brinker L.M., Madipu R., Kolonay J.F., Selngut J. Ren Q., Brinker L.M., Madipu R., Kolonay J.F., Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B., Shateman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A., Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E., Weinstcock G.M., Norris S.J., Frassr C.M., Paulsen I.T.; "Comparison of the genome of the oral pathogen Treponema denticola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Streptococcus agalactiae, a pathogen causing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%; Score 6; DB 2; Length 183; 100.0%; Pred. No. 14; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                   Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 AA; 21243 MW; 12A79C080C813D5C CRC64;
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                                                                                                                    OL-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein gbs1354.
OrderedLocusNames=gbs1354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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PBroc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
EMBL; AE017252; AAS12523.1; -
TIGR; PDE2009; -
                                                                                    183 AA
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PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
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EMBL; AL766850; CAD47013.1; -.
SagaList; gbs1354; -.
                                                                                  PRT;
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05-JUL_2004 (TrEMBLrel. 27,
05-JUL_2004 (TrEMBLrel. 27,
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invasive neonatal disease."
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Best Local Similarity luv...
6; Conservative
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                                                                                  PRELIMINARY;
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SEQUENCE 183 AA
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Q73L56;
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                                         RESULT 12
Q8E4P7
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85.7%; Score 6; DB 2; Length 261;

Query Match

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Dujon B., Sherman D., Fischer G., Nauveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
"Genome evolution in yeasts.",
I. Nature 430:35-44(2004).
                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosome C of strain NRRL Y-
1140 of Kluyveromyces lactis.
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                                                                                                                                                                                                               Kluyveromyces lactis NRRL Y-1140.
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Kluyveromyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 AA; 32546 MW; E6A28199F8830A06 CRC64;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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295 AA
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100.0%; Pred. No. 22;
:ive 0; Mismatches
PRT;
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InterPro; IPR010993; SAM_homology.
Pfam; PP00788; RA; 1.
SMART; SM00314; RA; 1.
PROSTITE; PS50200; RA; 1.
SEQUENCE 295 AA; 32546 MW; B6A
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PRELIMINARY;
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01-OCT-2000
01-JUN-2003
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Q9K764
ID Q9K76
AC Q9K76
DT 01-0C
DT 01-0U
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SEQUENCE FROM N.A.

C STRAIN=C-125;

WEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;

X MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;

X Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,

R Tomplete genome sequence of the alkaliphilic bacterium Bacillus

X Horikoshi K.;

Morplete genome sequence comparison with Bacillus subtilis.";

X Nucleic Acids Res. 28:4317-4331(2000).

ENBL; ABO01519; BAB07228.1; -.

R FNBL; ABO01519; Fendonuclease activity; IEA.

COMPLETE Protecome; Endonuclease.

X Complete protecome; Endonuclease.

X Complete protecome; Endonuclease.
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                  Bacillus halodurans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
OrderedLocusNames=BH3509;
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Search completed: November 7, 2005, 19:32:41 Job time : 5.71622 secs

142 SSQDYF 147

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Best Local Similarity 100.
Matches 7; Conservative
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Sequence 7, Appli
Sequence 10, Appl
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Sequence 4442, Ap
Sequence 14523, A
Sequence 166, App
Sequence 47564, A
Sequence 22820, A
Sequence 22820, A
Sequence 22814, A
Sequence 22814, A
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19796, A
22814, A
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12425, A
19369, A
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Sequence 7, Appli
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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S-09-902-540-12425
S-09-248-796A-19369
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US-09-270-767-47564
US-09-369-247-108
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US-09-583-110-4016
US-09-107-433-4442
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US-09-672-459-7
US-09-636-252A-10
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US-08-600-908A-10
US-08-683-838A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                     US-10-820-200-2_COPY_161_167
                                                                                           OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Word size :
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                               Seguence:
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   Sequence 167, App
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 628, Ap
Sequence 19304, A
Sequence 19304, A
Sequence 7, Appli
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Sequence 23640, A
Sequence 28424, A
Sequence 6596, Ap
Sequence 10404, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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COUNTRY: USA
ZIP: 10174-6401
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,899
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/343,804
FILING DATE: 22-NOV-1994
ATTONERY/AGENT INFORMATION:
US-09-369-247-167
US-08-143-219-25
US-08-436-711-9
US-08-436-711-9
US-09-949-016-6268
PCT-US-55-02058-9
US-09-248-796A-19304
US-09-248-796A-19304
US-09-248-796A-19304
US-09-371-913A-7
US-09-371-913A-7
US-09-97-805-7
US-09-134-000C-5895
US-09-134-000C-5895
US-09-252-991A-23640
US-09-252-991A-23640
US-09-252-991A-23640
US-09-252-991A-23640
US-09-955-991A-23640
US-09-958-991A-23640
US-09-958-991A-23640
US-09-99-016-6596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08720899; Patent No. 5753460; Patent No
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TELEPHONE: 212-867-0123
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 40
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: New York
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58308370 No. 5830837disk of No. 5830837th America, Inc.
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APPLICANT: Takada, Toshikazu
APPLICANT: Takada, Toshikazu
APPLICANT: Shimada, Jiro
APPLICANT: Wanase, Michiyo
APPLICANT: Yanase, Michiyo
APPLICANT: Yanase, Michiyo
APPLICANT: Takata, Hiroki
APPLICANT: Makata, Hiroki
APPLICANT: Okada, Shigetaka
TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
TITLE OF INVENTION: NEOPULULANASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
STREET: Metropolitan Square Building, Suite 800, 1450
STREET: Washington
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                                                                                                         COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: The PC-COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/343,804
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,715A
FILIAG DATE: 14-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 7; DB 2;
                       STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
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APPLICATION NUMBER: JP 306096/1993
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Patent No. 5965442
                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: LOWINGY Dr., Karen A.
REGISTRATION NUNBER: 31,274
REPERENCE/DOCKET NUMBER: 4054
TELECOMMUNICATION INFORMATION:
TELEFRAN: 212-867-0123
TELEFRAN: 212-867-0123
TELEFRAN: 212-869-9555
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acids
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US-08-343-804-7
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  ADDRESSEE: No.
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COMPUTER READABLE FORM: COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: PC POSS/MS-DOS
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APPLICATION NUMBER: US/08/459,610 FILING DATE: 02-UN-1995 CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PREDICATION NUMBER: US/08/43,804 FILING DATE: 22-NOV-1994 ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A. REGISTRATION NUMBER: 31,274 REGISTRATION NUMBER: 31,274 REGISTRATION INFORMATION:
TELEPHONE: 212-867-0123
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                                                                                                                                                    Sequence 7, Application US/08459610
Patent No. 5801043
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Thellersen, Marianne
TILLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
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Sequence 7, Application US/08343804

Sequence 7, Application US/08343804

Patent No. 5830837

GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITIE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
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SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 7; Conservative
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1 SSODYFH 7
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Gaps

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ADDRESSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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Fatent No. 6143708
GENERAL INFORMATION:
APPLICANT: Bvender, Allan
APPLICANT: Bagard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182,859
CURRENT PILING DATE: 1998-10-29
FARLIER APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-867-0123
                                                                                                                                                                                                | Sequence 10, Application US/08683838A | Sequence 10, Application US/08683838A | Setent No. 6022724 | General Information: Seendsen, Allan APPLICANT: Bisg rd-Frantzen, Henrik APPLICANT: Borchert, Toxben Vedel TITLE OF INVENTION: '-Amylase Mutants NUMBER OF SEQUENCES: 13 | CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 amino acids
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Best Local Similarity 100.
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STRANDEDNESS: single
                                     141 SSQDYFH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 SSODYFH 147
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                                                                                                                                                 RESULT 6
US-08-683-838A-10
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US-09-182-859-7
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APPLICANT: Bigg rd-Frantzen, Henrik
APPLICANT: Bigg rd-Frantzen, Locale and Least and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB.1996
CLASSIFICATION: 435
ATTOMREY/AGENT INPORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFRENCE/COCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                  NAME: Melser, Allen S.
REGISTRATION NUMBER: 27,215
REFERENCE/DOCKET NUMBER: 1835.009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-824-8000
TELEFK: 202-824-8199
TELEX: 246516
INFORMATION FOR SEQ ID NO: 2:
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Patent No. 5989169
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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CURRENT FILING DATE:
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                                                                                                                    SEQ ID NO 10
LENGTH: 478
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100.0%; Score 7; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Score 7; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 10, Application US/09636252A
Sequence 10, Application US/09636252A
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
ITILE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICERAL INCORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torban
APPLICANT: Bisgard-Frantzen, Henrik
IITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-03
FILE REFERENCE: 4796.204-03
FRIOR PELLOATION NUMBER: 09/182,859
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 0775/96
PRIOR PILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-11-08
NUMBER OF SEC ID NOS: 37
LENGTH: 478
LENGTH: 478
                 EARLIER FILING DATE: 1996-06-28
EARLIER APPLICATION NUMBER: 0775/96
EARLIER APPLICATION NUMBER: 07-11
EARLIER APPLICATION NUMBER: 1263/96
SARLIER PILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 478
EARLIER APPLICATION NUMBER: 0712/96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09672459
Patent No. 6436888
                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bacillus licheniformis US-09-672-459-7
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US-09-672-459-7
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GENERAL INCOMPATION:
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pheumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOD-07A
CURRENT APPLICATION NUMBER: 2009-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
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                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 7; DB 4; Best Local Similarity 100.0%; Pred. No. 0.27; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 4; 100.0%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGENERAL INCORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Bigard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-04-30
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-01-30
PRIOR FILING DATE: 1996-11-08
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PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FLING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/10186042; Patent No. 6642044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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Best Local Similarity 100.
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                                                                                                                                                                     TYPE: PRT
ORGANISM: A. oryzae
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APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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                                                      Gaps
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                                                   0; Indels
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       Length 95;
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Sequence 166, Application US/09369247

Sequence 166, Application US/09369247

GENERAL INPORMATION:

TITLE OF INVENTION: 44 Human Secreted Proteins

FILE REFERENCE: PEO24P1

CURRENT APPLICATION NUMBER: 06/074,118

EARLIER PILING DATE: 1999-08-05

EARLIER FILING DATE: 1998-02-09

EARLIER FILING DATE: 1998-02-09

EARLIER FILING DATE: 1998-02-09

EARLIER PLICATION NUMBER: 60/074,137

EARLIER PLICATION NUMBER: 60/074,137

EARLIER PLICATION NUMBER: 60/074,141

EARLIER FILING DATE: 1998-02-09

EARLIER FILING DATE: 1998-02-09

EARLIER FILING DATE: 1998-02-09

EARLIER FILING DATE: 1998-02-09

EARLIER PILING DATE: 1998-02-09
       DB 4;
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100.0%; Pred. No. 2...
0; Mismatches
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100.0%; Pred. No. 30;
iive 0; Mismatches
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; Sequence 14523, Application US/09248796A
; Patent No. 6747137
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans
Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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51 QDYFH 55
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US-09-369-247-166
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Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                       Length 84;
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: CURKOWN
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Unn-1998
PRIOR APPLICATION NUMBER: 60/085131
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ARTILISHO:
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                 Query Match 71.4%; Score 5; I Best Local Similarity 100.0%; Pred. No. Matches 5; Conservative 0; Mismatch
                                            PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4016
LENGTH: 84
  PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 100 Beaver Street
                                                                                                                                                                                                  TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (781)893-5007
TELEPRA: (781)893-8277
INFORMATION FOR SEQ ID NO: 4442:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 95 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5206
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                40 ODYFH 44
                                                                                                                                                                                                                                                                                                                                                                                                      3 ODYFH 7
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71.4%; Score 5; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels
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124 SQDYF 128
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1 SQDYF 5
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Search completed: November 7, 2005, 19:00:10 Job time : 2.05405 secs

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7, 2005, 18:58:04; Search time 3.74324 Seconds (without alignments) 782.441 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/NSO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

21: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

22: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

22: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1867879 segs, 418409474 residues
                                                                                                                                                                                                                                                                                               US-10-820-200-2_COPY_161_167
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                                                                                                                    OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                 November
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Perfect score:
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No.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Description	Sequence 43, Appl	Sequence 10, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 10, Appl	Sequence 7, Appli	Sequence 10, Appl	Sequence 22, Appl	Sequence 2, Appli	Sequence 30, Appl	Sequence 18, Appl	
score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution	SUMMARIES	CI.	US-10-877-849-43	US-10-184-771-10	US-10-186-042-7	US-10-644-187-7	US-10-926-720-10	US-10-980-759-7	US-11-064-196-10	US-10-815-495-22	US-10-820-200-2	US-10-877-849-30	US-10-815-495-18	
qua] BiB		DB	17	14	14	15	11	17	20	16	16	17	16	
an or e y analy		% Query Match Length DB	476	478	478	478	478	478	478	498	498	498	499	
ter thived b	d	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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9 2 3 3 3 3			Ϊ.	۵.					_	_	_	_		

Sequence 5, Appli Sequence 40, Appli Sequence 45, Appl Sequence 307,711, Sequence 325770, Sequence 135770, Sequence 135435, Sequence 18445, Sequence 18445, Sequence 113292, Sequence 113292, Sequence 287848, Sequence 226734, Sequence 226734, Sequence 21466, Appli Sequence 213791, Sequence 113791, Sequence 113791, Sequence 113791, Sequence 113791, Sequence 116789, Sequence 116789, Sequence 116789, Sequence 1167, Appli Sequence 1167, Appli Sequence 1166, Appli Sequence 1168, Appli	ì	1 476; 318 0; Gaps 0;
US-10-797-393A-5 US-10-877-849-40 US-10-877-849-40 US-10-228-063-45 US-10-425-115-307711 US-10-425-115-325770 US-10-424-599-12331710 US-10-424-599-153435 US-10-424-599-153435 US-10-424-599-164027 US-10-437-963-113292 US-10-425-115-287848 US-10-425-115-28789 US-10-425-115-319361 US-10-62-548-166 US-10-02-755-108 US-11-002-755-108 US-11-002-755-108	LIGNMENTS 9 FOR STARCH PROC 877,849	Score 7; DB 17; Length Pred. No. 2.7; 0; Mismatches 0; Indel
1174 - 177 - 178 -	US/108777 54071A1 0aki ko cobu cobu cten ten RENYM 00-US BER: US/11 004-06-25 ion 3.2	6.6
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ttion US/1 (050054071) Hircaki Rikako Shinobu Eric Caraten 1918en, A HYBRID I NUMBER: :: 2004-0 S: 3 204-0 S: 4 204-0 S: 1 104 oryza	10 10 vativ
	849-43 ida Application US/1087784 ion No. US20050054071A1 int: Udagawa, Hiroaki NT: Taira, Rikako NT: Tagai, Shinobu NT: Tkagi, Shinobu NT: Allain, Eric NT: Allain, Eric NT: Hjort, Carsten NT: Vikso-Nielsen, Anders F INVENTION: HYBRID ENZYMES FERENCE: 10490.500-US FILING DATE: 2004-06-25 OF SEQ ID NOS: 43 ER: Patentin version 3.2 OF SEQ ID NOS: 43 ER: Repergillus oryzae ER: EX: mat_peptide ON: (1)(476)	Similarity 7; Conserv. SSQDYFH 7         SSQDYFH 14
11111111111111111111111111111111111111		Query Match Best Local S Matches 7 Qy 1

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PRIOR APPLICATION DATA:
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| Sequence 7, Application US/10186042
| Publication No. US20030171236a1
| GENERAL INFORMATION:
| APPLICANT: Svendsen, Allan
| APPLICANT: Briggard-Frantzen, Henrik
| TITLE OF INVENTION: Alpha-Amylase Mutants
| FILE REFERENCE: 4796.204-US
| CURRENT APPLICATION NUMBER: US/10/186,042
| CURRENT FILING DATE: 2000-06-28
| PRIOR PLING DATE: 1996.204-US
| PRIOR FILING DATE: 1996-10-29
| PRIOR FILING DATE: 1996-00-21
| PRIOR PLING DATE: 1996-00-21
| PRIOR FILING DATE: 1996-07-11
| PRIOR FILING DATE: 1996-11-08
| NUMBER OF SEC ID NOS: 37
| SEC ID NOS: 37
                                                                               APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REPERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT PILING DATE: 2002-06-28
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
                  Sequence 10, Application US/10184771 Publication No. US20030170769A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: A. Oryzae
US-10-184-771-10
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-10-184-771-10
                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 10
LENGTH: 478
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US-10-186-042-7
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Sequence 17, Aprileation Usfy104(4187)

FURLIANT STREAM AND TOUR 1040(1040315)A.

GERREAL INFORMATION: Allaha Anylane Mutants

TITLE OF INVENTION: Allaha Anylane Mutants

FILE SPERRING: Allaha Anylane Mutants

SEQ ID NO 7

SEQ ID NO 7

SEQ ID NO 7

SEQ ID NO 8

10 SEGOTH 147

DD 141 SEGOTH 147

DD 141 SEGOTH 147

MUTANTS: Allaha Anylane Mutants

COMPETER: Anylane Companylane Mutants

FILE SPERRING: Allaha SPERRING: Allah
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GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
ITILE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
ITILE OF INVENTION: Matants Of Aspergillus Niger
ITILE OF INVENTION: Mutants Of Aspergillus Niger
CURRENT APPLICANT: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 498
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                                                                                                                                                                                                                                                                                                                              100.0%; Score 7; DB 20; Length 478; 100.0%; Pred. No. 2.7; ive 0; Mismatches 0; Indels
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; Publication No. US20040229764A1
; GENERAL INFORMATION:
    APPLICANT: Bisgard-Frantzen, Henrik
    APPLICANT: Bisgard-Frantzen, Henrik
    APPLICANT: Pedereen, Sven
    TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
    TILE REFERENCE: 5835.200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
    CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR PILING DATE: 2000-11-09
; PRIOR PILING DATE: 2000-11-06
; PRIOR PILING DATE: 1999-11-16
; WUMBER OF SEQ ID NOS: 5
; SSEQ ID NO 2
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/11/064,196
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PEASERQ for Windows Version 3.0
LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-10-815-495-22
Sequence 22, Application US/10815495
Publication No. US20040191864A1
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US-10-815-495-22
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Best Local Similarity 100...
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                          ; ORGANISM: A. oryzae
US-11-064-196-10
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  REFERENCE/DOCKET NUMBER: 4394.204-US
           TELECOMMUNICATION INDUMEN: 4594.204-

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 4'8 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-10-926-720-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1000-09-28
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Publication No. US20050118695A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
TITLE OP INVENTION: Alpha-Amylase Mutants
FILE REPRENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/980,759
CURRENT FILING DATE: 2004-11-03
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Publication No. US20050170487A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bacillus licheniformis US-10-980-759-7
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Best Local Similarity 100.v
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Best Local Similarity 100.0
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Sequence 40, Application US/10877849

Sequence 40, Application US/10877849

GENERAL INFORMATION:

APPLICANT: Udagaw, Hiroaki

APPLICANT: Taira, Rikako

APPLICANT: Taira, Rikako

APPLICANT: Aliain, Eric

APPLICANT: Hjort, Carsten

APPLICANT: Hjort
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100.0%; Score 7; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Dedersen, Sven
APPLICANT: Pedersen, Sven
APPLICANT: Pestersen, Sven
APPLICANT: Festersen, Rikke Monica
TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
FILE REFERENCE: 10391.200-US
CURRENT APPLICATION NUMBER: US/10/797,393A
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
LENGTH: 499
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                                                                                                                                                                        US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Artificial US-10-877-849-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5
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publication No. US20050054071A1
GENERAL INFORMATION:
APPLICANT: Udagawa, Hiroaki
APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Taira, Shinobu
APPLICANT: Taira, Eric
APPLICANT: Hjort, Carten
APPLICANT: Vikaco-Nielsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490.500-US
CURRENT APPLICATION NUMBER: US/10/877,849
CURRENT PILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEG ID NO 30
LENGTH: 498
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2
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; ORGANISM: Aspergillus oryzae
US-10-877-849-30
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; ORGANISM: Aspergillus niger
US-10-815-495-18
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Best Local Similarity 100."
Matches 7; Conservative
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161 SSQDYFH 167
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US-10-228-063-45
i Sequence 45, Application US/10228063
i Sequence 45, Application US/10228063
i Publication No. US20030135885A1
i GENERAL INFORMATION:
i APPLICANT: Lanahan, Mike
i TITLE OF INVENTION: Self-processing Plants and Plant Parts
if TIRE REPRENCE: 109846.317
i CURRENT APPLICATION NUMBER: US/10/228,063
i CURRENT FILING DATE: 2002-12-12
i CURRENT FILING DATE: 2002-12-12
i NUMBER OF SEQ ID NOS: 60
i SOFTWARE: FastSEQ for Windows Version 4.0
i SEQ ID NO 45
i LENGTH: 1095
i TYPE: PRT
i ORGANISM: Aspergillus shirousami
US-10-228-063-45
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100.0%; Score 7; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 7; DB 17; Length 640; Best Local Similarity 100.0%; Pred. No. 3.4; Matches 7; Conservative 0; Mismatches 0; Indels
APPLICANT: Tkagi, Shinobu
APPLICANT: Allain, Eric
APPLICANT: Hjorc, Careten
APPLICANT: Hjorc, Careten
APPLICANT: Vikeo-Nielsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
FILE REFERENCE: 10490.500-US
CURRENT APPLICATION WIMBER: US/10/877,849
CURRENT FILING DATE: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEQ ID NO 36
LENGTH: 640
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                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Artificial
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8, Appli 38, Appl 34, Appl 32, Appl 41, Appl 18, Appl 12469, A 14, Appl 15, Appl

Sequence Sequence

1, Appli 1, Appli 291647, 169831, 13129, A 12810, A 50236, A 284520,

Sequence Sequence Sequence Sequence Sequence Sequence

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Word size :

Database :

Perfect score:

Run on:

Sequence:

Scoring table:

125916, 129535

Sequence Sequence Sequence

Sequence Sequence Sequence

13, Appl 2223, Ap 45, Appl 42, Appl

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

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TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQFTAYGDAYHGYWQQDIYSLNENYGTADDL 120
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US-11-064-196-10
US-10-815-495-12
US-10-815-495-18
US-10-228-063-45
US-10-213-90-42
US-10-369-493-223
US-10-369-493-223
US-10-877-849-42
US-10-877-849-38
US-10-877-849-34
US-10-486-868-15
US-10-46-868-15
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al Similarity 100.0%; Score 498; Call Similarity 100.0%; Pred. No. 0; 498; Conservative 0; Mismatches
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US-10-820-200-2
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                                                                                                                                             7, 2005, 18:58:04; Search time 266.305 Seconds (without alignments) 782.441 Million cell updates/sec
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Sequence 36,
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Sequence 10,
Sequence 7,
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Sequence 1
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(cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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                      5.1.6
Compugen Ltd.
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US-10-877-849-30
US-10-877-849-40
US-10-877-849-43
US-10-877-849-43
US-10-1847-71-10
US-10-1847-171-10
US-10-926-720-10
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                        GenCore version
Copyright (c) 1993 - 2005
                                                                                                       OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                   November
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Gaps

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QY         241 KAAGUYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300           Db         241 KAAGUYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK 300           QY         301 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 360           Db         301 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 360           Db         301 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 360           QY         361 PANREATWLSGYPTDSELYKLIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGT 420           Db         361 PANREATWLSGYPTDSELYKLIASANAIRNYAISKOTGFVTYKNWPIYKDDTTIAMRKGT 420           CQ         421 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLP 480           Db         481 RVLYPTEKLAGSKICSSS 498           Db         481 RVLYPTEKLAGSKICSSS 498           Db         481 RVLYPTEKLAGSKICSSS 498	RESULT 3 US-10-797-393A-5  US-10-797-393A-5  Sequence 5, Application US/10797393A  Publication No. US20040219649A1  GENERAL INFORMATION:  APPLICANT: Pedersen, Sven  APPLICANT: Pedersen, Rike Monica  TILLE OF INVENTION: ALCOHOL PROCESSES  FILE REFERENCE: 10391.200-US  CURRENT APPLICATION NUMBER: US/10/797,393A  CURRENT APPLICATION NUMBER: US/10/797,393A  CURRENT APPLICATION NUMBER: 2004-03-10  NUMBER OF SEQ ID NOS: 5  SEQ ID NO 5  SEQ ID NO 5  TYPE: PRT  APPE: PRT  APPE: PRT  CURRENT APPLICATION OFFICE  CURRENT APPLICATION OFFICE  CURRENT FILING DATE: 2004-03-10  NUMBER OF SEQ ID NOS: 5  CURRENT FILING PASE  CURRENT APPLICATION OFFICE  CUR	, 9.8 ×	QY         121 KALSSALHERGMYLANDVVANHMGYDGAGSSVDYSVFRPFSSQDYFHPFCFIQNYEDGTQ 180           Db         122 KALSSALHERGMYLANDVVANHMGYDGAGSSVDYSVFRPFSSQDYFHPFCFIQNYEDGTQ 181           QY         181 VEDCWLGDNTVSLPDLDTTXDVVANHWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240           Db         182 VEDCWLGDNTVSLPDLDTTXDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240	Qy         241 KAAGUYCIGEVLDGDPAYTCPYQNVMDGVLAYPILAAFKSTSGSMDDLYNMINTVK 300           bb         242 KAAGUYCIGEVLDGDPAYTCPYQNVMDGVLAYPILYYPLLAAFKSTSGSMDDLYNMINTVK 301           Qy         301 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILANGIPIIYAGQEQHYAGGND 360           Db         302 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILANGIPIIYAGQEQHYAGGND 361           Qy         361 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTTAMRKGT 420           Db         362 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTTAMRKGT 420           Db         362 PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTTAMRKGT 421
Db 61 TWQGIIDKLDYIQGMGFTALWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120  Qy 121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFRPFSSQDYFHPFCFIQNYEDCTQ 180  121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFRPFSSQDYFHPFCFIQNYEDCTQ 180  121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFRPFSGDYFHPFCFIQNYEDCTQ 180  Qy 191 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFRPFSGDYFHPFCFIQNYEDCTQ 180  241 KAAGVYCIGEVLDGDPAYTCPYQNVADGVLNYPIXPLIANFKSTSGSMDDLYNMINTVK 300  Qy 241 KAAGVYCIGEVLDGDPAYTCPYQNVADGVLNYPIXPLIANFKSTSGSMDDLYNMINTVK 300  Qy 301 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQBQHYAGGND 360  Qy 301 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQBQHYAGGND 360  Qy 301 SDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQBQHYAGGND 360  Qy 301 PANREATWLSGYPDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT 420  DD 361 PANREATWLSGYPDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT 420  AS PANREATWLSGYPDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT 420		APPLICANT: VÍKBO-Nielsen, Anders TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING FILE REFERENCE: 10490.500-US CURRENT APPLICATION NUMBER: US/10/877,849 CURRENT FILING DATE: 2004-06-25 NUMBER OF SEQ ID NOS: 43 SEQ ID NO 30 LENGTH: 498 TYPE: PRT TYPE: PRT ORCANISM: Aspergillus Oryzae US-10-877-849-30	Query Match Best Local Similarity 100.0%; Score 498; DB 17; Length 498; Best Local Similarity 100.0%; Pred. No. 0; Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 NVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG 60	CART   CARTER   CAR

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241 KAAGUYCIGEVLDGDPAYTCPYQNVMDGVLNYPIXYPLLNAFKSTSGSMDDLYNMINTVK 300
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                                                    US-10-877-849-36

| Sequence 36, Application US/10877849|
| Publication No. US20050054071A1|
| GENERAL INPORMATION:
| APPLICANT: Taira, Rikako |
| APPLICANT: Taira, Rikako |
| APPLICANT: Taira, Rikako |
| APPLICANT: Hjort, Carsten |
| APPLICANT: Hjort, Carsten |
| APPLICANT: Alain, Eric |
| APPLICANT: Alain, Exit |
| APPLICANT: Alain, Exit |
| APPLICANT: Alain, Exit |
| APPLICANT: Vikeo-Nielsen, Anders |
| TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING |
| FILE REPERENCE: 10490-560-405 |
| CURRENT FILING DATE: 2004-06-25 |
| NUMBER OF SEQ ID NOS: 43 |
| SOFTWARE: Patentin version 3.2 |
| LENGTH: 640 |
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Mismatches
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tive 0; Mismatche
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Best Local Similarity 100.
Matches 498; Conservative
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US-10-877-849-43
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PANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGT
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                                                                                                                                                            us-10-877-849-40

is Sequence 40, Application US/10877849

is Publication No. US20050054071A1

is GENERAL INFORMATION:

is APPLICANT: Udagawa, Hiroaki

is APPLICANT: Taira, Rikako

is APPLICANT: Tragi, Shinobu

is APPLICANT: Allain, Eric

is APPLICANT: Vikeo-Nielsen

if TILLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING

if TILLE OF INVENTION: HYBRID ENZYMES

if CURRENT APPLICATION: HYBRID ENZYMES

if CURRENT PILING DATE: 2004-06-25

is UDRAGN: Patentin version 3.2

is SOFTWARE: Patentin version 3.2

is EQID NO 40

is LENGTH: 608
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100.0%; Score 498; L
Best Local Similarity 100.0%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches
                                                                              RVLYPTEKLAGSKICSSS 498
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ORGANISM: Artificial
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APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-07-30
PRIOR FILING DATE: 1996-07-30
PRIOR FILING DATE: 1996-07-31
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 478
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                                                                                                                                                    ; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10
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0;
                  APPLICANT: Udagawa, Hiroaki
APPLICANT: Taira, Rikako
APPLICANT: Traira, Rikako
APPLICANT: Traira, Shinobu
APPLICANT: Algai, Shinobu
APPLICANT: Hjort, Caraten
APPLICANT: Wikso-Nielsen, Anders
TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
TITLE REFERENCE: 10490.500-US
FILE REFERENCE: 10490.500-US
CURRENT APPLICATION NUMBER: 2004-06-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEQ ID NO 434
LENGTH: 476
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95.6%; Score 476; DE
Best Local Similarity 100.0%; Pred. No. 0;
Matches 476; Conservative 0; Mismatches
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FUBLICation No. US20030170769A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Biggard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TILLE REFRENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
CURRENT FILING DATE: 2002-06-28
FRIOR APPLICATION NUMBER: US/10/184,771
FRIOR APPLICATION NUMBER: US/10/184,771
FRIOR APPLICATION NUMBER: US/10/184,771
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43
GENERAL INFORMATION:
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US-10-184-771-10
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61 WITPVTAQLPQTTAYGBAYHGYMQODIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
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                                                                                                                                                                                                                                                                                                                                                      PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
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                                                                                                                     NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
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ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ASYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/926,720
FILING DATE: 26-AUG-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bisg+rd-Frantzen, Henrik
Borchert, Torben Vedel
TITLE OF INVENTION: -Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
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APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
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REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 43:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/10926720
Publication No. US20050019886A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
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TELEFAX: 212-878-9655
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Best Local Similarity
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US-10-926-720-10
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                                                    Query Match 78.5%; Score 391; DB 14; Length 478; Best Local Similarity 100.0%; Pred. No. 0; Matches 391; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Svendeen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Grantzen, Henrik
TILE OF INVENTION: Alpha-Amylase Mutants; TILE OF INVENTION: DATE: 1998-10-29; PRIOR FILING DATE: 1998-04-30; PRIOR FILING DATE: 1998-04-30; PRIOR PRIOR APPLICATION NUMBER: 0712/96; PRIOR APPLICATION NUMBER: 0775/96; PRIOR PLING DATE: 1996-07-11; PRIOR PLING DATE: 1996-07-11; PRIOR FILING DATE: 1996-07-11; PRIOR PLING DATE: 1996-07-11; PRIOR 
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US-10-644-187-7
US-10-186-042-7
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                                                        NHMGYDGAGSSVDYSVPKPFSSODYFHPFCFLONYEDOTOVEDCWLGDNTVSLPDLDTTK
                                                                                                                             PYONVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
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100.0%; Pred. No. 0;
ive 0; Mismatches
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APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen
CURRING BATE: 075-175-16
CURRENT FILING DATE: 2005-02-2
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR PILING DATE: 2000-08-10
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/11064196; Publication No. US20050170487A1; GENERAL INFORMATION:
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; ORGANISM: A. oryzae
US-11-064-196-10
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                                   ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
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Mismatches
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APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/980,759
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-0-29
PRIOR FILING DATE: 1996-0-30
PRIOR FILING DATE: 1996-0-30
PRIOR FILING DATE: 1996-0-30
PRIOR FILING DATE: 1996-0-11
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Publication No. US20050118695A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
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391; Conservative
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US-10-980-759-7
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; Pred. No. 0;
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2004-03-3
NUMBER OF SEQ ID NOS: 30
SOFWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 499
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Best Local Similarity 99.8%;
Matches 477; Conservative
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US-10-815-495-18
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US-10-228-063-45
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APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Mutants Of Aspergillus Niger
FILE REFERENCE: 10345, 200-US
CURRENT APPLICATION NUMBER: US/10/815, 495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
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Publication No. US20040191864A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
FILE REFERENCE: 10345.200-US
CURRENT APPLICATION NUMBER: US/10/815,495
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    PASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
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                                             LIASANAIRNYAISKOTGFVTYKNWPIYKDD
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                                                                                                                                                                                           Sequence 22, Application US/10815495 Publication No. US20040191864A1 GENERAL INFORMATION:
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US-10-815-495-22
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US-10-815-495-18
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LENGTH: 498
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Search completed: November 7, 2005, 19:22:49 Job time : 267.305 secs

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Query Match
Best Local Similarity 100.
Matches 391; Conservative
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Sequence 7, Appli
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S-10-186-042-7
S-09-189-060B-72
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S-09-189-060B-70
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S-09-672-459-7
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                                               GenCore version (c) 1993 - 2005
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Maximum DB seq length: 2000000000
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
STATE: New York
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30, Appl
42, Appl
50, Appl
52, Appl
60, Appl
64, Appl
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ZIP: 10174-6401

COUNTRY: USA

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/720,899

FILING APPLICATION: 435

PRIOR APPLICATION UMBER: US/08/343,804

FILING APPLICATION WHERE: 22-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: ATTORNEY/AGENT ATTORNEY
US-09-252-991A-25354
US-09-134-000C-4388
US-09-613-182-7
US-09-613-182-7
US-09-648-795A-25525
US-09-647-468-142
US-09-647-468-40
US-09-647-468-50
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US-09-647-468-64
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US-09-647-468-70
US-09-647-468-70
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APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
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NAME: LOWINGY Dr., Karen A.

REGISTRATION NUMBER: 31,274

REPERENCE/DOCKET NUMBER: 4054

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123

TELEFAX: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR ESQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acids
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Patent No. 5753460
GENERAL INFORMATION:
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478 amino acids
                              Query Match 78.5
Best Local Similarity 100.
Matches 391; Conservative
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 US-08-459-610-7
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APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendeen, Marianne
APPLICANT: Svendeen, Marianne
APPLICANT: Thellersen, Marianne
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AWYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.
STREET: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: DEADEN PC-DOS/MS-DOS
SOFTWARE: PREADIL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,610
FILING DATE: 02-JUN-1995
CLASSIFICATION BATA:
APPLICATION NUMBER: US 08/343,804
FILING DATE: Z2-NOV-1994
ATTORNEY/AGRET INFORMATION:
ANDARE: DEADENT NO PARAINED
                                                              WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
                                                                                   NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
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                  ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIOGMGFTAI
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Patent No. 5801043
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REGISTRATION NUMBER: 31,274
REGISTRATION NUMBER: 40574
RELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: aingle
TOPEL amino acid
STRANDEDNESS: aingle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: No. 58308370 No. 5830837disk of No. 5830837th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
                                                                                                                                               9
                                                                                                                                       1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                  21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                               Gaps
                                               ;
0
DB 1; Length 478;
                                               Indels
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ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,804
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78.5%; Score 391;
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APPLICANT: Borchert, Torben Vedel
APPLICANT: Svendsen, Allan
APPLICANT: Thellersen, Marianne
APPLICANT: Van der Zee, Pia
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5830837di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-NOV-1994
CLASSIFICATION.
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Patent No. 5830837
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: LOWINGY Dr., Karen A.
REGISTRATION NUMBER: 31, 274
REFERENCE/DOCKET NUMBER: 4054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-869-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 433
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APPLICATION NUMBER: US 06
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
             478 amino acide
                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 391; Conservative
                                                single
                                                                               ; MOLECULE TYPE: CDNA
US-08-600-908A-10
                           TYPE: amino acid
STRANDEDNESS: gir
TOPOLOGY: linear
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CLASSIFICATION:
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CITY: New York
CITY: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TOWN PC POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 121 NHMGXDGAGSSVDYSVFKPFSSQDYFHPFCF1QNYEDQTQVEDCWLGDNTVSLPDLDTTK
                                                                                                                                                                          21 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
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                                                                                                   78.5%; Score 391; DB 2; Length 478
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APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFRENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1999655
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APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Toben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 59891690 NO. 59891690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10. Application US/08600908A Patent No. 5989169 GENERAL INFORMATION:
                                                                                                                      100.08;
                                                                                                                  Best Local Similarity 100.
Matches 391; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
amino acid
RDNESS: single
                                          TOPOLOGY: linear
                         STRANDEDNESS
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US-08-600-908A-10
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STREET: 405 Lexington Avenue, 64th Floor
                                                                Gaps
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DB 2; Length 478;
                                                                0; Indels
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STATE: New York
COUNTRY: New York
COUNTRY: New York
COUNTRY: Now York
COUNTRY: Now York
COUNTRY: Now York
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 LIASANAIRNYAISKDTGFVTYKNWPIYKDD 411
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78.5%; Score 391; DB
100.0%; Pred. No. 0;
ive 0; Mismatches
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Patent No. 6022724
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Toxben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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LIASANAIRNYAISKDTGFVTYKNWPIYKDD 411
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APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Blegard-Frantzen, Henrik
APPLICANT: Blegard-Frantzen, Henrik
TTLE OF INVENTION: Alpha-Amylase Mutants
FTLE REFERENCE: 4796, 204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT APPLICATION NUMBER: 09/182,859
FRIOR FILING DATE: 1998-10-29
FRIOR FILING DATE: 1996-04-30
FRIOR FILING DATE: 1996-06-28
FRIOR FILING DATE: 1996-06-28
FRIOR FILING DATE: 1996-07-11
FRIOR APPLICATION NUMBER: 0775/96
FRIOR FILING DATE: 1996-07-11
FRIOR APPLICATION NUMBER: 0775/96
FRIOR FILING DATE: 1996-07-11
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
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; Patent No. 6436888
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; ORGANISM: Bacillus licheniformis
US-09-672-459-7
                        Best Local Similarity 100.
Matches 391; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
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APPLICANT: Svendeen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Blagard-Frantzen, Henrik
APPLICANT: Blagard-Frantzen, Henrik
TTLE OF INVENTION: Alpha-Amylaee Mutants
FILE REFERENCE: 4796.204.0S
CURRENT APPLICATION NUMBER: US/09/182.859
CURRENT FILING DATE: 1996-10-29
EARLIER FILING DATE: 1996-04-30
EARLIER APPLICATION NUMBER: 0712/96
EARLIER APPLICATION NUMBER: 0775/96
EARLIER APPLICATION NUMBER: 0775/96
EARLIER APPLICATION NUMBER: 1263/96
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
EARLIER FILING DATE: 1996-07-11
SEARLIER FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 377
SCOTWARRE: FRELERY FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 377
SECTION NO SEQ ID NOS: 377
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Patent No. 6143708
GENERAL INFORMATION:
                  TELEPHONE: 212-867-0123
TELEFAX: 212-878-9555
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 478 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 478
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-182-859-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 391, Conservative
                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-683-838A-10
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US-09-182-859-7
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61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSINBNYGTADDLKALSSALHERGMYLMVDVVA 120
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78.5%; Score 391; DB 3; Length 478; 100.0%; Pred. No. 0; 1.00.0%; Indels ive 0; Mismatches 0; Indels
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241 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
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                361 LIASANAIRNYAISKDTGFVTYKNWPIYKDD
381 LIASANAIRNYAISKDTGFVTYKNWPIYKDD
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US-08-339-715A-2
; Sequence 2, Application US/08339715A
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7 ORGANISM: Bacillus licheniformis
US-10-186-042-7
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61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
                                                DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
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100.0%; Pred. No. 0;
iive 0; Mismatches 0
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Fatent No. 6440716
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Scorchert, Torben Vedel
ITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
CURRENT FILING DATE: 2000-08-10
PRIOR PILING DATE: 2000-08-10
PRIOR PILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
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ORGANISM: A. oryzae
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2 MVAWWSLFLYGLQVAAPA 19
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Best Local Similarity 100.0
Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
                               APPLICANT: Dalboge, Henrik APPLICANT: Sandal, Thomas
Patent No. 6270968
GENERAL INFORMATION:
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US-09-189-060B-72
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US-09-189-060B-66
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US-09-189-060B-66
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                      APPLICANT: Takada, Toshikazu
APPLICANT: Takada, Toshikazu
APPLICANT: Takada, Toshikazu
APPLICANT: Shimada, Jinao
APPLICANT: Shimada, Jinao
APPLICANT: Shimada, Jinao
APPLICANT: Vanase, Michiyo
APPLICANT: Yanase, Michiyo
APPLICANT: Okada, Shigetaka
TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
TITLE OF INVENTION: ADRESS:
ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
STREET: Metropolitan Square Building, Suite 800, 1450
STREET: G. Street
CITY: Washington
STATE: D.C.
CCUNTRY: USA
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47.8%; Score 238; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-219;
Matches 238; Conservative 0; Mismatches 0; Indels
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RESULT 11 US-09-189-060B-72 ; Sequence 72, Application US/09189060B

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APPLICANT: Dalboge, Henrik
APPLICANT: Sandal, Thomas
APPLICANT: Sandal, Thomas
APPLICANT: Sandal, Thomas
APPLICANT: Sandal, Thomas
APPLICANT: Borge, Diderichsen
TILE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
FILE REFERENCE: 4772.204-US
CURRENT APPLICATION NUMBER: US/09/189,060B
CURRENT APPLICATION NUMBER: PS-11-10
PRIOR APPLICATION NUMBER: PCT/DK97/00216
PRIOR APPLICATION NUMBER: PCT/DK97/00216
PRIOR FILING DATE: 1997-05-12
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 306
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APPLICANT: Sandal, Thomas
APPLICANT: Sandal, Thomas
APPLICANT: Sandal, Thomas
APPLICANT: Borge, Diderichsen
TITLE OF INVENTION: Method of Providing No. 6270968el DNA Sequences
FILE REFERENCE: 4772.204-US
CURRENT APPLICATION NUMBER: US/09/189,060B
CURRENT FILING DATE: 1998-11-10
PRIOR FILING DATE: 1997-05-12
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US-09-189-060B-68

Sequence 68, Application US/09189060B

Sequence 68, Application US/09189060B

SEQUENCE No. 6270968

APPLICANT: Dalboge, Henrik

APPLICANT: Sandal, Thomas

APPLICANT: Rauppinen, Markus

APPLICANT: Borge, Diderichsen

TITLE OF INVENTION Method Of Providing No. 6270968el DNA Sequences

FILE REFERENCE: 4772.204-US

CURRENT APPLICATION NUMBER: US/09/189,060B
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100.0%; Pred. No. 6.2e-09;
tive 0; Mismatches 0; Indels
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Pred. No. 6.2e-09;
0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 304
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US-09-189-060B-74
is Sequence 74, Application US/09189060B
patent No. 6270968
is Patent No. 6270968
is GENERAL INFORMATION:
APPLICANT: Sandal, Thomas
APPLICANT: Sandal, Thomas
APPLICANT: Sandal, Thomas
APPLICANT: Markus
APPLICANTON WHERE: 1996-11-10
BRIOR FILING DATE: 1996-11-10
BRIOR FILING DATE: 1997-05-12
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 74
LENGTH: 307
THENGTH: 307
THENGTH: 307
THENGTH: 307
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US-09-189-060B-70

Sequence 70, Application US/09189060B

Sequence 70, Application US/09189060B

GENERAL INFORMATION:

APPLICANT: Dalboge, Henrik

APPLICANT: Sandal, Thomas

APPLICANT: Rauppinen, Markus

APPLICANT: Borge, Diderichsen

TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences

CURRENT APPLICATION NUMBER: US/09/189,060B

CURRENT FILING DATE: 1998-11-10

PRIOR FILING DATE: 1997-05-12

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 308
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3.6%; Score 18; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION WUBBR: PCT/DK97/00216
PRIOR FILING DATE: 1997-05-12
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 68
LENGTH: 306
TYPE: PRT
TYPE: PRT
US-09-189-0608-68
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US-09-189-0608-74
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 MVAWWSLFLYGLQVAAPALA......LPRVLYPTEKLAGSKICSSS 498 OLIGO Gapop 60.0 , Gapext 60.0 US-10-820-200-2 498 Perfect score: Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

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Word size :

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		4 4 4 4 4 4 0 4 5 6 4 7

## ALIGNMENTS

<b>Z</b> (	ALASI alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae N'Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
J O O & 3	C;Species Aspergillus Oryzae C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004 C;Accession: S04548; A33214; JS0240; A91930; A93767; A10627 R;Wirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
. 4444	out: hitching a part of a
******	A;Residues: 1-499 <wir> A;Cross-references: UNIPROT:P10529; EMBL:X12725; NID:g2430; PIDN:CAA31218.1; PID:g29592 A;Genetics: AWT1 A;Accession: A33214 A;Wolecile type: mRNA</wir>
4420	A;Residues: Î-499 <wi2> A;Cross-references: GB:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921 R;Genes, M.J.; Dove, M.J.; Seligy, V.L. Gene 79, 107-117, 1989</wi2>
444	A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin A;Reference number: JS0240; MUID:89378767; PMID:2789162
IAAAK	A;Molecule type: UNA A;Residues: 1-499 <gen> A;Genetics: AMY2 A;Note: the authors refer to this as isozyme II R;Isemura, S.; Ikenaka, T.</gen>
חממממ	J. Biochem. 74, 1-10, 1973 A;Reference number: A91930; MUID:74001521; PMID:4733850 A;Accession: A91930 A;Molecule type: protein A;Residues: 206-225 <ise></ise>
<u></u>	Proc. JD. 185-290, 1975 A;Reference number: A93767 A;Accession: A93767
<b>₹</b> ₹₽	A;Molecule Cype: procein A;Residues: 434-443,446-447,'Q',449-458,'GTTV',459-464,467-468,'B',470,'B',472-499 <nar *Matsuura, Y:, Kusunoki, M.; Harada, W.; Kakudo, M. T. Biocham OS. 607-707, 1904</nar 
	A;Tile: Structure and possible catalytic residues of Taka-amylase A. A;Tile: Structure and possible catalytic residues of Taka-amylase A. A;Keference number: A37454; MUID:84212370; PMID:660921 A;Contents: annotation; X-ray crystallography, 3.0 angstroms R;Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkenburg, J.P.; Wilkinson, A submitted to the Brookhaven Protein Data Bank, August 1992 A;Reference number: A51549; PDB:6TAA A;Reference number: A51549; PDB:6TAA A;Reference annotation; X-ray crystallography, 2.1 angstroms, residues 22-497 C;Comment: One atom of calcium per molecule is essential for activity.

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A;Gene: amy1
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Genetics: <aAMY2-A;Gene: amy2; Amy11
C;Genetics: <aAMY2-A;Gene: amy2; Amy11
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
A;Gene: amy2; Amy11
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pethway: glycogen/starch degradation
C;Superfamily: Agergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calclum; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polys
F;121/Domain: signal sequence #status experimental <AAT>
F;124/20main: alpha-amylase core homology <AMY>
F;121/Domain: alpha-amylase core homology <AMY>
F;159/31/10main: alpha-amylase core homology <AMY>
F;159/31/10main: alpha-amylase core homology <AMY>
F;142,183,196,231/Bainding site: calcium (Aan, Glu, Asp, Hstatus experimental F;142,183,196,231/Bainding site: calcium (Aan, Glu, Asp, #status experimental F;227,221,318/Active site: Asp, Glu, Asp #status predicted
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JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C;Species: Aspergillus sp.
C;Species: Aspergillus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C;Accession: JS0663
R;Shibuya, L.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shirousamii and its expression A;Reference number: JS0663; MUID:92323146; PMID:1368777
A;Accession: JS0663
A;Accession: JS0663
A;Residues: 1-499 <SHI>
C;Function:
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Appecies: Aspergillus awamori
C;Species: Aspergillus alpha-awylase genes
C;Accession: A48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Cxr.; Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-awylase genes from Asper A;Reference number: A48305
A;Accession: A48305
A;Accession: A48305
A;Accession: A48305
A;Accession: A48305
A;Cross-references: UNIPROT:Q02905
C;Function:
A;Bestives: Treferences: UNIPROT:Q02905
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C;Superfamily: Aspergillus alpha-amylase; alpha-awylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>
catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
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                             A Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Reywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-499/Froduct: alpha-amylase #status predicted <ALP>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;194-321/Domain: alpha-amylase core homology cany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 KAAGVYCIGEVLDVDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVK
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                                                                                                                                                                                                                                                                                                            Score 397; DB 2; Length 499;
Pred. No. 0;
0; Mismatches 1; Indels
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al Similarity 99.8%; Pre
497; Conservative 0;
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A;Molecule type: DNA
A;Residues: 1-499 «WIR»
A;Cross-treferences: UNIPROT:Q96TH4; EMBL:X12727; NID:g2454; PIDN:CAA31220.1; PID:g29592.
A;Accession: A33215
A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1499 kW12.

A; Residues: 1499 kW12.

A; Residues: 1499 kW12.

A; Crose-references: GB:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922

R; Genes, M.J.; Dove, M.J.; Sellgy, V.L.

Gene 79, 107-117, 1989

A; Title: Appergillus oryzae has two nearly identical Taka-amylase genes, each containing A; Reference number: J80240; MUID:89378767; PMID:2789162

A; Accession: A44713

A; Accession: A44713

A; Residues: 1-499 cGRN>
A; Rusunoki, M.; Harada, W.; Kakudo, M.
T; Libe: Structure and possible catalytic residues of Taka-amylase A.
A; Title: Structure and possible catalytic residues of Taka-amylase A.
A; Reference number: A37454; MUID:84212370; PMID:660921

A; Contents: annotation; X-ray crystallography, 3.0 angstroms
C; Genetics:
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C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C; Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; meta
F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 22-499/Product: alpha-amylase 3 #status experimental <MAT>
F; 194-321/Domain: alpha-amylase core homology <AMY>
F; 195-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F; 142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F; 218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 218,218,251,318/Active site: His, Glu, Asp #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-amylage (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
N;Alternate names: alpha-amylage isozyme I; glycogenase; Taka-amylage A
C;Species: Aspergillus oryzae
C;Species: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: 804549; A33215; Ā44713
K;Wirsel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon
A;Reference number: 804548; MUID:89237897; PMID:2785629
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                                                            SDCPDSTILLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGND 361
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A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
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Best Local Similarity 99.8
Matches 442; Conservative
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R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Circoman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asper A;Reference number: A48305; MUID:90254827; PMID:2340591
A;Recession: B48305
A;Retues: preliminary; not compared with conceptual translation
A;Residues: 1-499 - KOR>
A;Residues: 1-499 - KOR>
A;Cross-references: UNIPROT:002906
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pescription: catalyzes the degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>
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                                                                                                                                                                                                                                                                                                                                                                            182 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHYQKDFWPGYN 241
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Species: Aspergillus awamori
Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
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   red. No. 0;
Mismatches
      Pred. No.
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100.08;
   Best Local Similarity 100.
Matches 384; Conservative
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NiAlternate names: glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Species: Aspergillus oryzae
C;Species: Aspergillus oryzae
C;Species: Junar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JT0466
R;Tada, S; Jimura, Y; Gomi, K; Takahashi, K; Hara, S; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A;Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergia
A;Recence number: JT0466
A;Accession: JT
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Best Local Similarity 100.
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JUNDSB
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
Nighternate names: Taka-amylase A
Nighternate names: Taka-amylase A
C;Species: Appergillus oryzae
C;Date: 11-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JN0588
C;Accession: JN0588
A;Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for mu A;Recession: JN0588
A;Reterence number: JN0588; MUID:90128276; PMID:2612911
A;Accession: JN0588
A;Molecule type: mRNA
A;Residus: 1-499 4-720.
A;Residus: 1-490 4-720.
A;Residus: 1-404/3
C;Reywords: 91ycoprotein; 91ycosidase; hydrolase; polyasccharide degradation
C;Superfamily: Aspergillus alpha-amylase; hydrolase; polyasccharide degradation
C;Superfamily: Aspergillus alpha-amylase; hydrolase; polyasccharide degradation
C;Reywords: 91ycoduct: alpha-amylase core homology
C;Reywords: 91ycoduct: alpha-amylase core homology AMX>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
A;21/Ponain: alpha-amylase core homology AMX>
E;218/Binding site: carbohydrate (Asn) (covalent)
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59.4%; Score 296; DB 2; I
Best Local Similarity 99.6%; Pred. No. 3.8e-294;
Matches 496; Conservative 0; Mismatches 2;
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Jubbas 30-Jun 1991 #sequence_revision 30-Jun-1991 #text_change occidentalis)
C;Species: Schwanniomyces occidentalis
C;Species: Sol-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S06115
R;Strasser, A.W.M.; Selk, R.; Dohmen, R.J.; Niermann, T.; Bielefeld, M.; Seeboth, P.; T
Eur. J. Blochem. 184, 699-706, 1989
A;Title: Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the secr
A;Reference number: S06115; MUID:90032659; PMID:2806251
A;Accession: S06115
A;Cross-references: UNIPROT:P19269; EMBL:X16040; NID:g4882; PIDN:CAA34162.1; PID:g4883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-amylase (EC 3.2.1.1) precursor - yeast (Schwanniomyces occidentalis)
C;Species: Schwanniomyces occidentalis
C;Species: Schwanniomyces occidentalis
C;Accession: S2355
R;Wu, F.M.; Wang, T.T.; Hsu, W.H.
PEMS Microbiol. Lett. 82, 313-318, 1991
A;Title: The nucleotide sequence of Schwanniomyces occidentalis alpha-amylase gene. A;Reference number: S23355
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Pathway: glycogen/starch degradation C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology C; Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation F; 1-20/Domain: signal sequence #status predicted <SIG>F; 21-50/Product: alpha-amylase #status predicted <MAT>F; 21-50/Product: alpha-amylase core homology <AMY>F; 229/Domain: alpha-amylase core homology <AMY>F; 13-4, 229/Domain: alpha-amylase core homology <AMY>F; 13-4, 229/Domain: alpha-amylase core homology candom of the core of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.0%; Score 20; DB 2; Le
100.0%; Pred. No. 7.4e-12;
tive 0; Mismatches 0;
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100.0%; Pred. No. 7.8e-11;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 GIIDKLDYIQGMGFTAIWI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 QGIIDKLDYIQGMGFTAIWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 <u>QGIIDKLDYIQGMGFTAIWI</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.C
Matches 20; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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N.Alternate names: alpha-1, 4 glucanohydrolase
C.Species: Schwanniomyces occidentalis
C.Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Accession: S33921
R.Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
R.Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
A.Title: Molecular structure of the SWA2 gene encoding an AWX1-related alpha-amylase from A.Accession: S33921; MUID:93365041; PMID:8358835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternate names: glycogenase; Taka-amylase A C; Species: Aspergillus oryzae
C; Species: Aspergillus oryzae
C; Species: Aspergillus oryzae
C; Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C; Accession: JK0201
R; Toda, H; Kondo, K; Narita, K.
Proc. Jpn. Acad. 58B, 208-212, 1982
A; Title: The complete amino acid sequence of Taka-amylase A.
A; Reference number: JK0201
A; Molecule type: protein
A; Residues: 1-478 < *TOD>
A; Accession: JK0201
A; Molecule type: protein
A; Residues: 1-478 < *TOD>
A; Cross-references: UNIPROT: P10529
C; Comment: One atom of calcium per molecule is essential for the activity.
C; Comment: One atom of calcium per molecule.
C; Comment: See also PIR:JT0466 and PIR:JS0240.
C; Comment: See also PIR:JT0466 and PIR:JS0240.
C; Comment: Catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Pathway: glycogen/starch degradation
C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology C; Keywords: glycoprotein; glycoside plane: amylase core homology c; Keywords: glycoprotein; glycoside plane: A; Pathway: Glycoside plane: A; Pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 DIYSLNENYGTADDLKALSSALHERGMYLMYDVVANHMGYDGAGSSVDXSVFKPFSSQDY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 FHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 FHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRI 205
            SGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKI 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYICPYQNVMDGVLNYPIYYPLLNAFKST 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 DIVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKST 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDG 343
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47.8%; Score 238; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 7.6e-235;
Matches, 238; Conservative. 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pha-amylase (EC 3.2.1.1) - Aspergillus oryzae
                                                                                                                                             CSSS 498
                                                                                                                                                                                                                                                           CSSS 499
                                                                                                                                       495
                                                                                                                                                                                                                                                           496
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Length 512 0; Indels

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A Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Pathway: glycogen/starch degradation C; Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology C; Eywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation F; 1-25/Domain: signal sequence #status predicted <SIG>F; 26-512/Product: alpha-amylase #status predicted <MAT>F; 209-316/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                             Length 512;
                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                             Score 19;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
A; Gene: AMY1
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A,Molecule type: DNA
A,Residues: 1-507 <CLA>
A,Residues: 1-507 <CLA>
A,Cross-references: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g3965
C,Fenetion:

Gaps

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C;Species: Aspergillus niger
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35282
C;Accession: A35282
R;Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pete
Biochemistry 29, 6244-6249, 1990
Biochemistry 29, 6244-6249, 1990
A;Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom x
A;Reference number: A35282, MUID:91002514; PMID:2207069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trans. A;Molecule type: mRNA
A;Residues: 1-484 <BOE>
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C;Species: Thermoactinomyces vulgaris
Cjate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 831478
R;Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; Histofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; Histofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; Histofemeister, B.; Mayer, G.; Heese, C.; Hansen, G.; Histofemeister, B.; Mayer, G.; Heese, G.; Hansen, G.; Histofemeister, B.; Mayer, G.; Histofemeister, G.; Hansen, G.; Histofemeister, G.; Hansen, G.; Histofemeister, G.; Hansen, G.; Histofemeister, G.; Histofemeister, G.; Hansen, G.; Histofemeister, G.; Hansen, G.; Hansen, G.; Histofemeister, G.; Histofemeister, G.; Hansen, G.; Histofemeister, G.; Histofeme
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A;Residues: 1-482 <HOF>
A;Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:g48289; PIDN:CAA49465.1; PID:g48290|
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A;Pathway: glycogen/starch degradation C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core degradation C;Reywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation F;173-300/Domain: alpha-amylase core homology <AMY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris
C;Species: Thermoactinomyces vulgaris
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;194-319/Domain: alpha-amylase core homology <AMY>
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Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 9.7e-06;
iive 0; Mismatches 0;
Score 16; DB 1; Li
Pred. No. 1.1e-07;
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-amylase (EC 3.2.1.1) - Aspergillus niger
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     Query Match
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Pullulanase (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)
Nyllulanase (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)
Nyllulanase (EC 3.2.1.41)
Nyllulanase (EC 3.2.1.41)
Cycordania alpha-daxtrin endo-1, 6-alpha-glucosidase (EC 3.2.1.41)
Cycordania alpha-daxtrin endo-1, 6-alpha-glucosidase (EC 3.2.1.41)
Cypecies: Lipomyces kononenkoae endo-1, 6-alpha-glucosidase (EC 3.2.1.41)
Cypecies: Lipomyces kononenkoae endo-1, 6-alpha-glucosidase (EC 3.2.1.41)
Cypecies: Lipomyces kononenkoae endo-1, 6-alpha-1996 #text_change 09-Jul-2004
Cypecies: Lipomyces analysis and expression in yeasts of a cDNA containing a Lipomyces for endo-1, 6-65-71, 1995
Ayreference number: Joyana endo-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6-100-1, 6
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C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004
C;Accession: T38770
R;Skelton, J; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: 221751
A;Accession: T38770
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-513 <SKE>
A;Genetics:
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LECURIO. C. C. Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

C. -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

R. EMBL; AB109452; BA010151.1; -..

R. GO; GO:0005952; P:alpha-amylase activity; IEA.

R. GO; GO:0005955; P:arbhydrate metabolism; IEA.

R. GO; GO:0005955; P:arbhydrate metabolism; IEA.

R. InterPro; IPR006049; Alpha amyl cat.

DR. InterPro; IPR006046; Glyco hydro.

DR. Pfam; PF00128; Alpha-amylase; 1.

DR. Pfam; PF00128; Alpha-amylase; 1.

DR. SMART; SM00642; Aamy; 1.

SEQUENCE 498 Aa; 54679 MW; 8407BBFC7F4E3FC0 CRC64;
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SEQUENCE FROM N.A.
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AMYA ASPNG
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Maximum DB seq length: 200000000
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MEDLINE=74001521; PubMed=4733850;
Isemura S., Ikhanka T.,
The amino acid sequences of glycopeptides obtained from Taka-amylase A with trypsin and chymotrypsin.";
                                                                                 421 DGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPWAGGLP
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                                                                                                                                                                                                                                                                                                                                                                      P10529; P11763; Q00250; O100250; O10027-1989 (Rel. 12, Created) O1-0CT-1989 (Rel. 12, Last sequence update) O5-0CT-2004 (Rel. 45, Last sequence update) Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-alpha-D-glucan glucanohydrolase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toda H., Kondo K., Narita K.;
"The complete amino acid sequence of Taka-amylase A.";
Proc. Jpn. Acad., B. Phys. Biol. Sci. 58:208-212(1982)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97428212; PubMed-9283074; DOI=10.1021/bi970539i;

MEDLINE-97428212; PubMed-9283074; DOI=10.1021/bi970539i;

MEZOZOWSKI A.M., Davies G.J.;

Bracozowski A.M., Davies G.J.;

Thiblitor acarbose at 2.0-A resolution.";

Brachemistry 36:10837-10845(1997).

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

Ilnkages in oligosaccharides and polysaccharides.

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

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CATALYTIC Monomer.

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

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CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

ILNKages in the starch industry to make high maltose and high DE

CATALYTIC ACTIVITY: In the starch industry to make high maltose and high DE

CATALYTIC ACTIVITY: Endohydrolyses of the alpha-yosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                   MEDLINE=80227691; PubMed=6156152;
MatEnura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
Toda H., Narita K., Kakudo M.;
"Molecular structure of taka-amylase A. I. Backbone chain folding at
3-A resolution.";
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Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
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MEDLINE=64212370; PubMed=6609921;
Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
"Structure and possible catalytic residues of Taka-amylase A.";
J. Biochem. 95:697-702(1984).
                                                                                                                                                             Phys. Biol. Sci. 51:285-290(1975)
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InterPro; IPR006589; Alp amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
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EMBL, X12726, CAA31219.1; --
EMBL, X12727; CAA31220.1; --
EMBL, D00434; BAA0336.1; --
EMBL, M33218; AAA32708.1; --
EMBL, M3218; AAA32708.1; --
PIR, JT0466; JT0466.
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6TAA; X-ray; @=22-499.
7TAA; X-ray; @=22-499.
Biochem. 74:1-10(1973)
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                                                                    TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL 120
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                                             TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
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MEDLINE=92323146; PubMed=1368777;

MEDLINE=92323146; PubMed=1368777;

MEDLINE=92323146; PubMed=1368777;

MEDLINE=92323146; PubMed=1368777;

"Cloning of the aupha-amylase CDNA of Aspergillus shirousamii and its expression in Saccharomyces cerevisiae ";

Biosci. Biochem. Sci174-179(1992).

-I. CATALYTIC ACTIVITY: Endohydrolysis of 1.4-alpha-glucosidic

Inkages in oligosaccharides and polysaccharides.

-I. COPCTOR: Binda 2 calcium inons per subunit. Calcium is inhibitory at high concentrations (By similarity).

-I. SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                  MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5070;
 Length 499;
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01-APR-1993 (Rel. 25, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OUT-2004 (Rel. 45, Last annotation update)
31-OCT-2004 (Rel. 45, Last annotation update)
32-OCT-2004 (Rel. 45, Last annotation update)
33-OCT-2004 (Rel. 45, Last annotation update)
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F -> L (in AMY3).
TT -> DC (in Ref. 5).
D -> Y (in Ref. 5).
D -> Y (in Ref. 3).
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                                                  InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR0066047; Alpha_amyl_cat.
InterPro; IPR0066047; Alpha_amyl_cat.
InterPro; IPR0060646; Glyco_hydro_13.
Pram; PF00128; Alpha-amylase; 1.
SMART; SMO642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                  218 N-linked (GlcNac. . .) (By similarity)
54852 MW; IFB7AE50DA01C03F CRC64;
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Calcium 1 (By similarity).
Calcium 1 (Wi carbonyl oxygen) (By similarity).
Calcium 1 (Via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (Via carbonyl oxygen) (By similarity).
Calcium 2 (By similarity).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 499;
                                                                                                                                                      Alpha-amylase.
Nucleophile (By similarity).
Proton donor (By similarity)
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99.8%; Pred. No. 0;
tive 0; Mismatches
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Matches 497; Conservative
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                                                                                                                                                                                                             Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
                                                                                                                                                                                                                                                                                                                                                      STEALN=KT-11;

Matsubara T.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

-: SUMILARITY: Belongs to family 13 of glycosyl hydrolases.

R GO; GO:0004555; F:alpha-amylase activity; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR06649; Alpha amyl cat sub.

R InterPro; IPR06649; Alpha amyl cat sub.

R InterPro; IPR06649; Alpha amyl cat sub.

R PRINTS; PR00128; Alpha-amylase; 1.

PRINTS; PR00110; ALPHAAMYLASE.
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                                           (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Matches 497; Conservative
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                                                                                                                                     Alpha-amylase precursor
                                                                                                                                                                                            Aspergillus awamori.
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                                                                                                                                                                                                                                             Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
"Cloning, characterization, and expression of two alpha-amylase genes
from Aspergillus niger var. awamori.";
Curr. Genet. 17:203-212(1990).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
                                                                                                                                                                                                                                                                                                                                    linkages in oligosaccharides and polysaccharides.
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR006589; Alp amyl_cat_sub.
Interpro; IPR006047; Alpha amyl_cat.
Interpro; IPR006047; Alpha amyl_cat.
Interpro; IPR006046; Glyco_hydro_13.
PRINTS; PR00110; ALPHAAMYLASE.
SWART; SM0642; Aamy; 1.
Galctum-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Multigene family; Signal.
                                                                                                                      Aspergillus awamori.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleophile (By similarity).

Proton donor (By similarity).

By similarity.
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
Calcium 2 (By similarity).
Similarity).
Calcium 2 (By similarity).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .linked (GlcNAc. . .) (Potential).
7658511BC01A8A01 CRC64;
                                           01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase A precursor (RC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.1%; Score 384; DB 1; Length 498;
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                  498 AA
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                  STANDARD;
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218
498 AA;
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                                                                                                    glucanohydrolase A)
Name≈AMYA;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Gaps

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Indels

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0; Mismatches

100.08;

Conservative

Best Local Similarity Matches 384; Conserv

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                                                                                                                                       121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
                                                                                                                                                            122 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
                                                                                                                                                                                                            181 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
                                                                                                                                                                                                                             182 VEDCWIGDNIVSLPDLDTIKDVVKNEWYDWVGSLVSNYSIDGLRIDIVKHVQKDFWPGYN
                2 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
                                                                    TWOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
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MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=105351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       499 AA
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InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 PANREATWLSGYPTDSELYKLIAS 385
                                                                                                                                                                                                                                                                                                                                                                                                                            PANREATWLSGYPTDSELYKLIAS 384
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01-0CT-1996 (Rel. 34, Last seq
25-0CT-2004 (Rel. 45, Last ann
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Q02906;
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57 KYCGGTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYG 116
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                                                                                                                                                                       Laiosci. Biotechnol. Biochem. 64:816-827(2000).

Li SintlaITY: Belongs to family 13 of glycosyl hydrolases.

EMBL; AB021876; BAA95703.1; -...

EMBL; AB021876; BAA95703.1; -...

PIR; JN0588; JN0588.

PIR; 504549; ALAS3.

RISSP; P10529; 7TAA.

GO; GO:0004556; F:alpha-amylase activity, IEA.

GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

RO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

RO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

RO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

RO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

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RO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

RO; GO:0016798; F:hydrolase activity, acting of glycosyl bonds; IEA.

RO; GO:0016798; F:hydrolase activity; IEA.

RO; 
                                                                                           characterization of a transcriptional activator
MEDLINE=20289310; PubMed=10830498; Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N., Limura Y., "Molecular cloning and characterization of a transcriptional activator gene, amyR, involved in the amylolytic gene expression in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 EDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 WPGYNKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKAVAAFIILNDGIPIIYAGQEQHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 AGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYCGGTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 TADDLKALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDF
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Aspergillus flavus.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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Pred. No. 0;
0; Mismatches 1; Indels
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Last annotation update)
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Matches 442; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPPSSQDYFHPFCFIQNYEDQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                      SMART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                        (By
                                                                                                                                                                                                                                                                                                                                                                                                                                (By
                                                                                                                                                                                                                                                                                                                                                     Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (B similarity).
Calcium 2 (By similarity).
By similarity.
Whinked (GlCNAC. ..) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                              Alpha-amylase B.
Nucleophile (By similarity).
Proton donor (By similarity).
By similarity.
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen) (similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Taka-amylase A (EC 3.2.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.1%; Scor.
100.0%; Pred. No. v,
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PANREATWLSGYPTDSELYKLIAS 384
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PRINTS; PR00110; ALPHAAMYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 384; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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599
185
185
296
186
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318
142
183
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499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-RIB40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5062;
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227
251
318
142
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171
261
461
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ACT_SITE
ACT_SITE
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355

356 415

235 236 295 296 416 475

Q96TH4;

**Q96TH4** 

RESULT 7 Q96TH4

ö 115

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Pfam; PF00128; Alpha-amylaBe; 1.
PRINTS; PR00110; ALPHAAMYLASE.
  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=27300;
                                                                                                                                                                                                                                                                                                                                                                                           DEBOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=SWA2;
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AMY2_DEBOC
                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415
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                                                                                                                                                                                                                                                                                                                                                                              116 TADDLKALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296
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                                                                                                                                                                                                                                                                                                                                                                                                                                EDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEMYDWVGSLVSNYSIDGLRIDTVKHVQKDF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPGYNKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNM 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHY 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 INTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHY 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 MRKGTDGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPM 476
                                            Fakhoury A.M., Woloshuk C.P.;

T "Amyl, the alpha-amylase gene of Aspergillus flavus: Involvement in aflatoxin biosynthesis in maize kernels.";

L bhytopathology 89:908-914(1999).

C -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

E MBL; AF139925; AAF14264.1; --.

R GO; GO:0004556; F:alpha-amylase activity; IEA.

R GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.

R InterPro; IPR006647; Alpha amylase and amylase.

R InterPro; IPR006699; Alpa amylase.

R InterPro; IPR006699; Alpa amylase.

R Pfam; PF00128; Alpha-amylase; 1.

R Pfam; PF00128; Alpha-amylase; 1.

R Pfam; PF00128; Alpha-amylase.

R Pfam; PR00128; Alpha-amylase.

R PRINTS; PR001101, AlphaAMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPGYNKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNM
                                                                                                                                                                                                                                                                                                                                                                                                                                              EDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDF
                                                                                                                                                                                                                                                                                                                                                                                              117 TADDLKALSSALHERGMYLAVDVVANHAGYDGAGSSVDYSVFKPFSSQDYFHPFCLIQNY
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                                                                                                                                                                                                                                                                                                     Gaps
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Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
[1]
                                                                                                                                                                                                                                                                          Length 499;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                   499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                          68.7%; Score 342; DB 2; 99.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623 AA
                                                                                                                                                                                                                                                                                                     0; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGLPRVLYPTEKLAGSKICSSS
                                                                                                                                                                                                                                                                                       Best Local Similarity 99.8
Matches 442; Conservative
                                                                                                                                                                                                                         SMART; SM00642; Aamy; 1.
Glycosidase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                          SEQUENCE FROM N.A.
 NCBI_TaxID=5059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Boase N.A., Murphy R.L., Kelly J.M.;
Boase N.A., Murphy R.L., Kelly J.M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-- Similarization and the control of glycosyl hydrolases.

EMBL; AF208214; AAF17100.1;

R HSSP; P56711; 2AAA.

GO; GO:0004556; P:alpha-amylase activity; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro: IPR006647; Alpha_amyl_cat.

InterPro: IPR006646; Alpha_amyl_cat.

InterPro: IPR006046; Glyco_hydro_la.

R InterPro: IPR006046; Glyco_hydro_la.

R InterPro: IPR006689; Alpha-amylase; 1.

R Pfam; PF00128; Alpha-amylase; 1.

R Pfam; PF00168; Alpha-amylase; 1.

R PRINTS; RR00110; ALPHAMYLASE.

R PRINTS; RR00110; ALPHAMYLASE.

R PRODOM; PD001568; CBM ZO; 1.

R SWART; SM00642; Aamy; 1.

C SEQUENCE 623 AA; 68598 MW; 822F002C37F5A9A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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25-0CT-2004 (Rel. 45, Last annotation update)
Alpha-amylase 2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.6%; Score 23; DB 2; Le
100.0%; Pred. No. 2.2e-13;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P10529; 7TAA.
InterPro; PR006589; Alp amyl_cat_sul
InterPro; IPR006047; Alpha amyl_cat_
InterPro; IPR006046; Glyco_hydro_13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 WRSQSIYFLLTDRFARTDGSTTA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 WRSQSIYFLLTDRFARTDGSTTA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2004 (Rel. 43, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similaricy
hes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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512 AA

STANDARD;

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          Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
Hydrolase; Signal.
                                                                                                                                                     (B)
                                                                                                                                                                                                                      (By
                                                                                                              By similarity.
Calcium 1 (By similarity).
Calcium 1 (Via carbonyl oxygen) (B similarity).
Calcium 1 (Via carbonyl oxygen) (B calcium 2 (By similarity).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                           (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boase N.A., Murphy R.M., Kelly J.M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
EMBL; AF208225; AAF17103.1; -.
HSSP; P10529; 77AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%; Score 19; DB 2; Length 490; 100.0%; Pred. No. 1.6e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           4.0%; Score 20; DB 1; Length 507;
                                                               Alpha-amylase 2.
Nucleophile (By similarity).
Proton donor (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                          -linked (GlcNac. . .) (P) 3A562E95BD8AAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54249 MW; A891C4ACEAEB5305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-YAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             1.7e-10;
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tive 0; Mismatches
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SEQUENCE 490 AA; 54
   Aamy;
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RESULT 12 AMY1\_DEBOC

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SEQUENCE FROM N.A.

Nucleotide Sequence of the extracellular alpha-amylase gene in the monorable sequence of the extracellular alpha-amylase gene in the structure for the extracellular alpha-amylase gene in the care for the structure f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 26076;
MEDIINE=90032659; PubMed=2806251;
Strasser A.W.M., Selk R., Dohmen R.J., Niermann T., Bielefeld M.,
Seeboth P., Tu G., Hollenberg C.P.;
"Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the secretion of its gene product in transformants of different yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CCRC 21164;
MEDLINE=92120467; PubMed=1769525; DOI=10.1016/0378-1097(91)90280-N;
Wu F.M., Wang T.T., Hsu W.H.;
"The nucleotide sequence of Schwanniomyces occidentalis alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
                                                                                                                                                                                                                                                                                Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis). 
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; 
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                         01-NOV-1990 (Rel. 16, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
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Nucleophile (By similarity).
Proton donor (By similarity)
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or send an email to license@isb-sib.ch).
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InterPro; IPR006047; Alpha amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; Alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
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     Created)
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PIR; S23355; S23355.
HSSP; P10529; 7TAA.
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SEQUENCE FROM N.A.
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MEDLINE=2184401; PubMed=11859360; DOI=10.1038/nature724;
MOOU V., Guilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
MOOURS W., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Collins S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., MoDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblet D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
Rutherford K., Rutter S., Saunders B., Seger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreage E., Rieger M., Schaefer M., Mieller-Auer S.,
Gabel C., Fuons M., Fritzc C., Lehrach H., Reinhardt R., Pohl T.M.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Berzym K., Jamerann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Albert B., Waller S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
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Constrain CCRC 21164 and strain Arc 26077)
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Constrain CCRC 21164
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STANDARD; PRT; 513 AA.
044154, 0874R5; 096K6;
11-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Probable alpha-amylase meu30 precursor (EG 3.2.1.1) (1.4-alpha-D-glucan glucanohydrolase) (Meiotic expression up-regulated protein 30).
Name-amd55; Synonyme-ameu30, ORFNAmes-SPACA5H1.09, SPAC4A8.01;
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetase;
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By similarity.
Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By calcium 1 (via carbonyl oxygen) (By
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                                                                               similarity).
Calcium 2 (By similarity).
N-linked (GlCNAC. . .) (Probable)
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857552B2CF60F965 CRC64;
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1.7e-09;
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                                                                                                                                                                                                                                                                                                            3.8%; Score 19; DB 100.0%; Pred. No. 1.7; ive 0; Mismatches
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Best Local Similarity 100.*
Matches 19; Conservative
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NCBI_TaxID=4896;
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512 AA;
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Ducas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 29:2327-2337(2001).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
-!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
at high concentrations (By similarity).
-!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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GeneDB SPombe; SPAC25H1.09; -.
InterPro; IPR006689; Alpha_amyl_cat.
InterPro; IPR006689; Alp_amyl_cat_sub.
Pfam; PF00128; Alpha-amylase; 1.
SWART; SM00642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                   MEDLINE=21270454; PubMed=11376151; DOI=10.1093/nar/29.11.2327; Watanabe T., Miyashita K., Saito T.T., Yoneki T., Kakihara Y., Nabeshima K., Kishi Y.A., Shimoda C., Nojima H.; "Comprehensive isolation of meiosis-specific genes identifies novel porteins and unusual non-coding transcripts in Schizosaccharomyces pombe.";
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Calcium 1 (By similarity).

Calcium 2 (By similarity).

Calcium 1 (via carbonyl oxygen) (By similarity).

Calcium 2 (By similarity).

Calcium 2 (By similarity).

By similarity.

By similarity.
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Calcium 1 (By similarity).
Calcium 1 (via carbonyl oxygen)
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Probable alpha-amylase meu30.
Nucleophile (By similarity).
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Pred. No. 1.7e-09;
0; Mismatches 0;
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Z98762; CAB11471.1; -.
EMBL, Z88944; CAD62442.1; -.
EMBL, ABD654314; BAB60880.1; -.
PIR, T38770; T38770.
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Search completed: November 7, 2005, 19:32:38
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Matches
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Q6YF33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P10529; 77AA.
InterPro; PR060689; Alp amyl cat sub.
InterPro; IPR066497; Alpha amyl cat.
InterPro; IPR066497; Alpha amyl cat.
InterPro; IPR066497; Alpha amyl cat.
Pfam; PF03170; CBM 21; 1.
SWART; SW06642; Aamy; 1.
Calcium-binding; Carbohydrate metabolism; Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                             MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0; Steyn A.J.C., Marmur J., Pretorius I.S.; "Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lipomyces kononenkoae alpha-amylase-encoding gene."; Gene 166:65-71(1995).
                                                                                                                                                                                                                       Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Lipomycetaceae, Lipomyces.
NCBI_TaxID=34357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family. -!- SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
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Calcium 1 (By similarity).
Calcium 2 (By similarity).
Calcium 1 (via carbonyl oxygen) (By similarity).
Similarity).
Calcium 2 (By similarity).
By similarity).
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Carbohydrate binding type-21.
Nucleophile (By similarity).
Proton donor (By similarity).
By similarity.
Calcium 1 (By similarity).
Calcium 1 (yia carbonyl oxygen) ()
                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
12-OCT-2004 (Rel. 45, Last annotation update)
Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase 1).
                                          624 AA.
                                          PRT;
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PIR; JC4510; JC4510.
                                          STANDARD;
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STRAIN=IGC4052B;
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Name=LKA1;
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Saccharomycetales, Lipomycetaceae, Lipomyces.
NCBI_TaxID=29829;
                                                                        (Potential).
 By similarity.
By similarity.
By similarity.
N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
87EB16534F5A9A9F CRC64;
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EMBH: AXIL55463; AAN75021.1; -- HSSP; P26827; 1A47.
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Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
Moon T.-W.;
                                                                                                                        Length 624;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                           Score 16; DB 1; Le
Pred. No. 1.8e-06;
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GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR005036; CBM 21.
Pfam; PF00128; Alpha-amylase; 1.
Pfam; PF03370; CBM_21; 1.
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100.0%; Fre
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                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-amylase.
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05-JUL-2004
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A. fumiga Amino aci

N-termina Amino aci Variant

Bacterial

Aaw44270 H Aaw44271 H Aaw44271 H AAD80178 A AAD80128 A AAD12899 A AAD12899 A AAD12899 A AAD9907896 A AAD9907896 A AAD9186 A AAD9186 A AAD9186 A AAD9186 A

Alpha-amy Variant a Variant a

Variant

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Run on:

Title: Perfect score:

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syrups, particularly of high maltose content, or alcohol, from starch; dough improver for baked goods; in brewing, to increase fermentability the wort; and for liquefaction of starch
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100.0%; Pred. No. 0;
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Best Local Similarity 100.
Matches 498, Conservative
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                                    Sequence 498 AA;
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Variant alpha amylase enzymes which have improved washing and/or as detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile desizing prior to scouring, bleaching and dyeing. The variants have improved thermostability, acid/alkaline stability, low temperature optimum; pH optimum; higher hydrolysis velocity and improved tolerance to other composition constituents, e.g. oxidation agents. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYQNVMDGVLNYPIYYPLLINAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ATPADWRSQSIYFLLIDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                       New Bacillus derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                     Ξ
                                                     Thellersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                     Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.5%; Scor.
100.0%; Pred. No. o,
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 391; DB
Pred. No. 0;
                                                                                                                                                                                                                                                                      Disclosure; Page 75-76; 105pp; English.
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                                                     Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR78270 standard; protein; 478
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Matches 391; Conservative
(NOVO ) NOVO-NORDISK AS
                                                                                                                                    WPI; 1995-161790/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 478 AA;
                                               chert TV, B
Der Zee P;
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for

alpha corresponding

parent

Toft

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66. .84
/label= loop 2 modification region
/label= loop 2 modification region
/note= "at least one amino acid residue of a parent alpha
-amplase (used as a template for a variant) corresponding
to 44-57 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 117-185 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28. .42.
/label= loop 1 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 12-19 of AAW1449 is deleted or replaced with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121. .181
//note= "at least one amino acid residue of a parent alpha -amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-206 of AAW14499; claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12. .38
/label= loop 1 modification region
/note= "preferred region where at least one amino acid
residue of parent alpha-amylase (used as a template for
a variant) corresponding to 14-15 of AAW14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a templace for a variant) corresponding to 48-51 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                             /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 8-18 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template fo a variant) corresponding to this fragment is deleted or
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/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template a
variant) corresponding to 121-181 of AAW14499 is
deleted or replaced with a fragment corresponding to tl
fragment; claim 26"
                             alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl; Aspergillus oryzae; Bacillus amyloliquefaciens; altered property; calcium dependency; substrate binding; stability; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction; sweetener; ethanol production; variant.
                                                                                                                                                                                                                                                                                                                               fragment corresponding to this fragment; claim 33
                                                                                                                                                                                                                                                                        /note= "at least one amino acid residue of a par
-amylase (used as a template for a variant) corr
to 7-23 of AAM14499 is deleted or replaced with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= loop 2 modification region
                                                                                                                                                                                                                                                          modification region
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Aspergillus oryzae alpha-amylase (mature protein)
                                                                                                                                                                                                                                                                                                                                                                             modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment; claim 32"
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                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                     .3. .45
'label= loop 1
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                                                                                                                                                                                                                                                                                                                                                                                           Oxidation stable alpha amylases can be used for the simultaneous desizing and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or Asp. The parent alpha amylase is pref. derived from a Bacillus species, although alpha amylases of fungal oxigin can also be used. This sequence is the wild type (unmodified) alpha amylase of Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 PYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
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                                                                                                                                                                                                                                                                                             simultaneous desizing or starch derivs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 478;
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starch
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0,
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                                                                                                                                                                                                                                                                                               stable alpha-amylase
                                                                                                                                                                                                                                                                                                                scouring of fabrics contg.
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 25-26; 37pp; English
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100.0%;
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les 391; Conservative
                                                                                                                                                                      (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                Marcher D,
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                                                                                           05-OCT-1994;
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                                                    10-AUG-1995
                                                                                                                                                                                                                                                                                           Use of an bleaching
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Matches

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RESULT 4

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/note= "preferred region where at least one amino acid
residue of a parent alpha amylase (used as a template for
a variant) corresponding to 196-198 of AAW14499 is
deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                     /note= "at least one amino acid residue of a parent alpha -amylase (used as a template for a variant) corresponding to 322-346 of AAW14498 is deleted or replaced with a fragment corresponding to this fragment; claim 36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the mature Aspergillus oryzae alpha-amylase (A). Variants of parent termamyl- and fungamyl-like alpha-amylases (and methods of constructing them) are claimed. Examples of variants are featured above. The variants have altered properties such as calcium dependency, substrate binding and stability. Also one or more proline or cysteine residues in the variant is modified or replaced with a non-proline or non-cystein residue such as alanine. The variants can be used for (dish)washing, as detergent additives or for fabric desizing or starch liquefaction. They can also be used for the production of sweeteners and ethanol from starch. See also AAW14498-99
                                                                                                                                                                                                                                 /note= "an amino acid fragment corresponding to this region is deleted from the parent sequence of a variant Fungamyl; claim 43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-amylase variants and methods of production - have altered properties such as calcium dependency, substrate binding and stability.
 replaced with a fragment corresponding to 102-199 of AAW14499; claim 42"
                                                                                               fragment corresponding to this fragment; claim 21/166. 173
/label= loop 3 modification region
                                                                                                                                                                                                                                                                           /label= loop 8 modification region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borchert TV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 87-88; 171pp; English
                                                                                                                                                                                                      fragment; claim 23<sup>1</sup>
181. .184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bisgard-Frantzen H,
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95DK-00001192.
95DK-00001256.
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                            Misc-difference
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23-OCT-1995;
10-NOV-1995;
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The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type biological substance. The medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance and second nucleotide sequences comprising modification of glucomytase (glash) and recovering heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase A (amyA) protein.
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                                                                                                                                                                                                                                                                                                                Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
1 ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI
                                                             61 WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                   NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCF1QNYEDQTQVEDCWLGDNTVSLPDLDTTK
                                                                                                                                                                                         DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK
                                                                                                                                                               DVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC
                                                                                                                                                                                                                               PYQNVMDGVL,NYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
                                                                                                                                                                                                                                                              PYONVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPR
                              WITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus niger neutral alpha-amylase A (amyA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glucoamylase; glaA; amyA; alpha-amylase A; enzyme.
                                                                                                                                                                                                                                                                                                                                                                  LIASANAIRNYAISKDTGFVTYKNWPIYKDD 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADT89632 standard; protein; 498
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N-PSDB; ADT89631.
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ATPADWRSQSIYFLIDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 21

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Length 478; 0; Indels

DB 2;

Score 391; DB; Pred. No. 0; 0; Mismatches

78.5%; Sca ilarity 100.0%; P: Conservative 0;

Query Match Best Local Similarity Matches 391; Conserv

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biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide sequences comprising modification of glucosmylase (glaA) and recovering heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase B (amyB) protein.
                                                                                                                                                                                                                                                                                                                                                                                          Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
                                                                                                                                                                                                                                                            TWQGIDKLDYIQGMGFTAIMITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
                                                                                                                                                                                                                                              KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
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                                                                                                                                                                                               TWOGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
                                                                                                                                                                                                                                                                                              VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
                                                                                                                                              MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-2002; 2002WO-US027129.
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N-PSDB; ACC44572.
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                                                                                                          Similarity
                                                                        Sequence 499 AA
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                                                                                                                                                          KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ
                                                                                                                                                                      VEDCHLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN
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                                                                                  MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGG
                                                                                                          TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDL
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                                    384; Conservative
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N-PSDB; ADT89627.
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                        Similarity
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Mature taka-amylase A.

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The present invention describes polynucleotides which encode processing enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose isomerase, or glucoamylase) that are optimised for expression in plants. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic processing enzymes, which are activated under suitable conditions to act upon the desired substrate. Also described are self-processing transgenic plants and plant parts, e.g. grain, which express one or more of these enzymes and have an altered composition that facilitates plant and grain or starch-derived products in a transformed plant part (TPP), by activating the starch processing enzyme contained in it. Transgenic grain is useful or produce food products naving improved taste and to produce fermentable substrates for ethanol and fermented beverages. (M) eliminates the need to mill or physically disrupt the integrity of plant parts prior to recovery of starch-derived products. The present sequence represents alpha-amylase/glucoamylase fusion procein, which is given in the
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                Novel polynucleotide encoding hyperthermophilic processing enzymes e.g. alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.
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                                                                                               Claim 1; Page 107; 158pp; English.
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Best Local Similarity 99.8
Matches 477; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1095 AA;
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(first entry)

22-MAR-1996

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 DIVKHVQKDFWPGYNKAAGVYCIGEVLDGDFAYTCPYQNVMDGVLNYPIYYPLLNAFKST 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the mature form of taka-amylase from A. oryzae. This sequence was used in a method for the generation of mutant pullulanases for use in the food industry (see also AAR79026-28). The wild type pullulanase enzyme was modified by the method of the invention for enhancing the hydrophobicity of a selected site of the pullulanase. The method comprises replacement of a group in the selected site with a hydrophobic group, replacement of an amino acid with a hydrophobic and/or insertion or deletion of a hydrophobic amino acid from the selected site. The method was used to produce neopullulanases Y377F,
                           stearothermophilus; mutant; food industry; replacement insertion; deletion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDG 323
                                                                                                                                                                                                                                                                                                                                                                                                         Modifying a transferase by enhancing hydrophobicity of a selected site increases transfer activity, also new mutant neo-pullulanase(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 FHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTVKHVOKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYONVMDGVLNYPIYYPLLNAFKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRI
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 10-11; 18pp; English
                                                                                                          Location/Qualifiers
                             Wild type; neopullulanase; B. modification; hydrophobicity;
                                                                                                                                                                                                                                                                    94JP-00288658
                                                                                                                                                                                                                                                                                                 93JP-00306096
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                                                                                                                         30. .38
150. .164
240. .283
439. .474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                             (NIDE ) NEC CORP.
(EZAK ) EZAKI GLICO CO.
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                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-279919/37.
                                                                           Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 478 AA;
                                                                                                                       Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                      JP07177891-A.
                                                                                                                                                                                                                                                                  31-OCT-1994;
                                                                                                                                                                                                                                                                                                 12-NOV-1993;
                                                                                                                                                                                                                                   18-JUL-1995.
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18-JUL-1994
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ID AAR4
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AC AAR4
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DT 25-M
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complete. Manufacturing maltogenic amylase comprises the following steps:

(1) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC 5027BP) and inserting the gene into plasmid putl19 to construct recombinant DNA (pThMA119); (ii) inserting the recombinant DNA to the for 10 hours in Luria-Bertani (LB) media and centrifuging the media to obtain a microbial cell; (iii) suspending the microbial cell with buffer solution at pH 7.5 and obtaining supernatant; and (iv) passing the supernatant through column chromatography and obtaining purified maltogenic amylase. The maltogenic amylase is a dimer comprised of two maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase consists of anino acid residues of credion that consists of amino acid residues of spro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn131, Glu1322, Val1329, and Hisla60. The present sepresents happergillus oryzae TARA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 IGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDST 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes manufacturing maltogenic amylase (EC 3.2.1.133) having improved transglycosylation activity, comprising using crystallisation and the three dimensional structure of maltogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoded by the preregion and the 5' part of the structural gene for the TAKA-amylase.
Thermus sp. 1M6501, maltogenic amylase; EC 3.2.1.133; crystallisation;
protein co-ordinate data; 3 dimensional structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 IGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 188; 196pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP70311 standard; protein; 46 AA.
                                                                                                                                                                                                                                                                                                                                                       99KR-00039130
                                                                                                                                                                                                                                                                                                                                                                                                                                               SAMYANG GENEX CORP.
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(revised)
(first entry)
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Matches 73; Conservative
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                                                                                        Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 423 AA;
                                                                                                                                                        KR2001027418-A.
                                                                                                                                                                                                                                                                                      09-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                       09-SEP-1999;
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25-MAR-2003
18-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SAMY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP70311

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant alpha-amylase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for use in detergents, dishwashing agents and liquefaction agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence os that of the Asoergillus oryzae alpha amylase, sold commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amylase exhibits a better activity level and better stability in the presence of oxidiaing agents than previous mutant alpha amylases, and improved thermostability at moderately low pH. The enzyme can be used as an additive for detergents, dishwashing agents and liquifaction agents. (Updated on 25-MAR-2001 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 STLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANRE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 LGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 LGDNTVSLPDLDTTKDVVKNEMYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 YCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 YCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                    Methionine substitution, stability, activity, detergent, dishwashing agents, liquifaction agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.4%; Score 226; DB 2; Le
100.0%; Pred. No. 2.7e-207;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Svendsen A, Bisgard-Frantzen H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB09072 standard; protein; 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 7; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               92DK-00000946.
92DK-00001503.
93DK-00000292.
                                                                                                                                                                                                                                                                                                                                                                                  93WO-DK000230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-048855/06.
                                                                                                                                                                                    Aspergillus oryzae.
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Matches 226; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUL-1992;
16-DEC-1992;
15-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1993;
                                                                                                                                                                                                                                                    WO9402597-A1
                                                                                                                                                                                                                                                                                                                     03-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The DNA was prepared from mycelium from A. niger DSM 2761. It was screened with a hybridsation probe from TAKA-amylase cDNA and two hybridising clones were found. Plasmids pNA1 and pNA2 each carry the full length amylase gene with promoters and upstream activating sequences. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                           Prodn. of proteins in Aspergillus – using promoter and upstream activating sequences derived from Aspergillus niger amylase genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast promoter; expression vector; TAKA-amylase; alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of TAKA-amylase signal and mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.0%; Score 45; DB 1; Le
100.0%; Pred. No. 7.1e-35;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Woeldike HF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR24437 standard; protein; 46 AA.
                                                                                                                                                                                                                                                                                        Fig 2; page 2/11; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .21
/label= signal
                                                           88WO-DK000145
                                                                                      87DK-00004609
87DK-00005126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92EP-00104421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86DK-00001226
                                                                                                                                                                                             WPI; 1989-085543/11.
N-PSDB; AAN91273, AAN91274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus oryzae; Hw325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Christensen T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
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                                                                                                                                     (NOVO ) NOVO IND AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ24569
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-1986;
                                                           02-SEP-1988;
                                                                                        04-SEP-1987;
                                                                                                      29-SEP-1987;
WO8901969-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-2003
25-MAR-2003
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                            09-MAR-1989
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                                                                                                                                                                 Woldlike H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR24437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent claims a process for the production of protein products in Aspergillus oryzaca and a promoter for use in Aspergillus. The process enables industrial production of many different polypeptides and proteins in A. oryzae. Examples of such products are chymosin or prochymosin and other rennets, proteases, lipases and amylases. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus niger neutral alpha-amylase including preregion as encoded by plasmids pNal and pNA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                Expressing proteins, esp. enzymes, in Aspergillus oryzae - by transforming with recombinant vector, pref. contg. the TAKA amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus niger DSM 2761; neutral alpha-amylase; presequence;
plasmid pNA1; plasmid pNA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 46; 7.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGS 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-terminal portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.0%; Score 45; DB 100.0%; Pred. No. 7.1
                                                                                                                                                                                                                                                                                                        Woeldike HF;
                                                                      Location/Qualifiers
1. .21
22. .46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .21
/note= "Preregion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP94631 standard; protein; 46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 39pp; English.
                                                                                                                                                                                                                                                                          (NOVO ) NOVO TERAPEUTISK LAB AS
                                                                                                                                                                                                                           86DK-00001226,
87DK-00001353,
                                                                                                                                                                                              87EP-00103806
           Aspergillus gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                         Aspergillus oryzae, Hw325,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
1es 45; Conservative
                                                                                                                                                                                                                                                                                                        Christensen T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .46
                                                                                                                                                                                                                                                                                                                                   WPI; 1987-265414/38.
N-PSDB; AAN70507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                   promotor system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46 AA;
                                                                                                                                                                                              16-MAR-1987;
                                                                                                                                                                                                                             17-MAR-1986;
17-MAR-1987;
                                                                                                                                                                 23-SEP-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
01-JUL-1990
                                                                                                                                   EP238023-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP94631;
                                                                        Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                        Boel E,
                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Gaps

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Length 46; Indels 45 46 The sequences given in ABB80164-87 show enzymatic proteins derived from

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The DNA whose sequence is in AAQ24569 was derived from the TAKA- amylase clone. It was inserted in BamHI digested pBR322 to give plasmid pTAKA 17. In pTAKA 17 the A. oryzae derived DNA is shown as a 5.5 kb BamHi/Sau 3AI - BamHI/Sau 3AI fragment, the promoter and upstream activating sequences representing a 2.1 kb fragment. In the method according to the present invention the sequence from nucleotide -1144 to nucleotide -10 has been used as one example of a well functioning part of the promoter region. In another embodiment of the present invention the nucleotide sequence from nucleotide - 1176 to -1 was preceded by the still not sequenced 1.05 kb fragment from pTAKA 17. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PI field.)
                                        Promoter providing efficient protein prodn. in Aspergillus - is the TAKA amylase promoter, opt. with activating sequences, giving high yields of
                                                                                               amylase promoter, opt. with activat homologous or heterologous enzymes.
                                                                                                                                                                                                                                        Disclosure, Fig 1, 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46 AA;
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Gaps ö 1 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGS 45 DB 2; Length 46; 0; Indels 7.1e-35; 9.0%; Score 45; DB 100.0%; Pred. No. 7.1 live 0; Mismatches Best Local Similarity 100. Matches 45; Conservative Query Match ઠે

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2 MVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGS 46

g

ABB80177 standard; protein; 495 AA RESULT 14 

11-AUG-2003 (first entry) ABB80177;

fumigatus AfAAL1.

beta-galactosidase; invertase; lipase; alpha-amylase; laccase; polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose; glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose; glyceride; starch; maltodextrin; oxidated phenolic compound; polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage; textile; tea liquor; cleaning ability. Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;

Aspergillus fumigatus.

WO2003012071-A2.

13-FEB-2003

05-AUG-2002; 2002WO-US024842.

03-AUG-2001; 2001US-0309870P

(ELIT-) ELITRA PHARM INC.

Novel isolated Aspergillus fumigatus polypeptide, useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents. ) N-PSDB; ABQ80345, ABQ80346. 2003-332729/31

Bussey H;

Storms R, Roemer T,

Jiang B,

Claim 17; Page 134-35; 169pp; English.

The sequences given in Assertance order activity of an enzyment control of an enzyment control of a tenname, cellulase, glucose oxidase, glucose, phytase, betacaet glucoset, cellulase, glucose oxidase, glucoset, phytase, betacaet galacturonase or xylanase. Compositions comprising the tannase are polygalacturonase or xylanase. Compositions comprising the tannase and composition to modulating the amount of compounds that comprise a galaate effect linkage in a composition. Compositions comprising the amount of composition composition composition. Composition composition composition composition composition composition composition composition composition. Composition composition composition composition composition composition composition composition. Composition composition composition composition composition composition composition composition composition. Composition compo ö particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions Gaps ö 4.6%; Score 23; DB 6; Length 495; 100.0%; Pred. No. 8.2e-13; ive 0; Mismatches 0; Indels 23; Conservative Local Similarity Sequence 495 AA; Query Match Matches ò

원

ADP19639 standard; peptide; 20 AA. ADP19639; RESULT 15 ADP19639

Aspergillus oryzae fungamyl signal peptide sequence.

09-SEP-2004 (first entry)

filamentous fungus; signal peptide; fungamyl

Aspergillus oryzae.

WO2004050695-A2.

17-JUN-2004.

05-DEC-2003; 2003WO-DK000838. 

05-DEC-2002; 2002DK-00001875.

(NOVO ) NOVOZYMES AS.

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Hansen TM;
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WPI; 2004-450719/42.

Producing a polypeptide of interest in a filamentous fungus comprises providing a modified DNA sequence by inserting a DNA sequence encoding one or more amino acid residues in between 2 DNA sequences.

Disclosure; SEQ ID NO 3; 36pp; English.

The invention relates to a method of producing a polypeptide of interest in a filamentous fungus comprising providing a modified DNA sequence by inserting a DNA sequence encoding one or more amino acid residues in between a DNA sequence encoding a polypeptide of interest and the adjacent upstream DNA sequence encoding the N-terminal signal peptide. The methods, DNA sequence, DNA construct and expression vector are useful for producing a polypeptide of interest. This sequence corresponds to the signal peptide sequence from the Aspergillus oryzae fungamyl protein used for producing the polypeptide of interest by the method of the invention.  $\mathbf{x}$   $\mathbf{x}$ 

Sequence 20 AA;

0; Gaps Query Match
4.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels

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1 MVAWWSLFLYGLQVAAPALA 20

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1 MVAWWSLFLYGLQVAAPALA 20

Search completed: November 7, 2005, 19:27:54 Job time : 288.494 secs

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7, 2005, 18:25:16; Search time 4.09459 Seconds (without alignments) 661.194 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          2105692 seqs, 386760381 residues
                                                                                                                                                                     US-10-820-200-2_COPY_161_167
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
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                                                                                                          November
                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                         Scoring table:
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Maximum DB
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s: \* geneseqp2003as: \* geneseqp2003bs: \* geneseqp20048: \* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* A Geneseq 16Dec04:\* geneseqp1980s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	ion	Aspergill	Mutant al	Aspergill	Aspergill	Mature ta	Aspergill		Aspergill	Aspergill	Alpha-amy	Alpha-amy			Arabidops	Arabidops	Human ORF	Human pol	Human adi	S. domunc	Human nuc		Rat MEGF1	Antipsori	PRO polyp	Streptoco
	Description	Abb09072	Aar46065	Aar72450	Aar78270	Aar79025	Aaw14500	Aab84206	Adt89632	Adt 89628	Abp96630	Aar88212	Aao08447	Aag36453	Aag36452	Aaq36451	Abp08801	Aao05772	Abu70873	Ado58298	Adg76988	Adj 78494	Adq42622	Adn05042	Adp25302	Adk47501
	ព	ABB09072	AAR46065	AAR72450	AAR78270	AAR79025	AAW14500	AAB84206	ADT89632	ADT89628	ABP96630	AAR88212	AA008447	AAG36453	AAG36452	AAG36451	ABP08801	AA005772	ABU70873	AD058298	ADG76988	ADJ78494	ADG42622	ADN05042	ADP25302	ADK47501
	DB	4	~	~	~	~	N	4	ω	œ	9	~	4	m	m	ო	Ŋ	4	9	æ	7	æ	7	8	æ	8
	Match Length DB	423	478	478	478	478	478	498	498	499	1095	493	52	1222	1257	1275	116	124	342	379	2112	3124	4351	82	82	84
*	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	92.5	85.0	85.0	85.0	85.0	82.5	82.5	82.5	82.5	82.5	82.5	82.5	80.0	80.0	80.0
	Score	40	40	40	40	40	40	40	40	40	40	37	34	34	34	34	33	33	33	33	33	33	33	32	32	32
11111	No.	<b>п</b>	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Abp42992 Human ova			Adh45430 Human mol	Abu44715 Protein e	Abp98616 Mature Er	Abp98615 Erwinia c	Ado61605 Transcrip	Abg15126 Novel hum	Abb70891 Drosophil	Aaw26654 Human PAN	Abg72922 Novel hum	Abm81509 Tumour-as	Adp25358 PRO polyp	Aab56501 Human pro	Adk62434 Disease t	Aay33673 B. bassia	Aam79737 Human pro
ADR95807	ABP42992	ADM92084	ABP28341	ADH45430	ABU44715	ABP98616	ABP98615	AD061605	ABG15126	ABB70891	AAW26654	ABG72922	ABM81509	ADP25358	AAB56501	ADK62434	AAY33673	AAM79737
<b>ω</b> ι	n u	ο α	Ŋ	œ	v	9	9	8	4	4	~	9	œ	8	m	7	N	4
95	180	180	182	195	323	326	348	351	501	529	583	583	583	583	594	685	700	715
80.0	0.0	80.0	80.0	80.0	80.0	90.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0
32	2 5	35	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
26	28	0 0	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation; protein co-ordinate data; 3 dimensional structure. Aspergillus oryzae TAKA protein (TAA). ABB09072 standard; protein; 423 AA. 99KR-00039130. 99KR-00039130 (POST-) POSTECH FOUND. (SAMY-) SAMYANG GENEX CORP. (first entry) WPI; 2001-534477/59. Aspergillus oryzae. Park GH; KR2001027418-A. 26-JUN-2002 09-SEP-1999; 09-SEP-1999; 06-APR-2001. ABB09072; Kim TJ, RESULT 1 ABB09072 

Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.

Disclosure; Page 188; 196pp; Korean.

The present invention describes manufacturing maltogenic amylase (EC 3.2.1.133) having improved transglycosylation activity, comprising using crystallisation and the three dimensional structure of maltogenic amylase. Manufacturing maltogenic amylase comprises the following steps: (i) obtaining a gene of maltogenic amylase from Thermus sp. 1M6501 (KCTC 5027BP) and inserting the gene into plasmid pUCI19 to construct recombinant DNA (pThMA119); (ii) inserting the recombinant DNA to Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius for 10 hours in Luria-Bertani (LB) media and centrifuging the media to sobtain a microbial cell; (iii) suspending the microbial cell, with buffer solution at pH 7.5 and obtaining supernatant; and (iv) passing the substrate through column chromatography and obtaining purified maltogenic amylase. The maltogenic amylase is a dimer comprised of two

141 SSQDYFH 147

SSODYFH

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AAR72450 standard; protein; 478 AA.
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                                                                      AAR72450
ID AAR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant alpha-amylase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for use in detergents, dishwashing agents and liquefaction agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      commercially as FUNGANYI (TW) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amin acid other than cysteine. The mutant alpha-amylase exhibits a better activity level and better stability in the presence of oxidising agents than previous mutant alpha amylases, and improved thermostability at moderately low pH. The enzyme can be used as an additive for detergents, dishwashing agents and liquifaction agents. (Updated on 25-MAR-2003 to correct PM Field.)
         (ThWA) crystal. The amylase has a structure containing an activated region that consists of amino acid residues of Asp-328, Glu-357, Asp-424, and a pocket with glucose bound that consists of amino acid residues of Pro44, Tyr45, Arg81, Arg83, Pro118, Cy8116, Ash1331, Glu1332, Val1329, and His1360. The present sequence represents Aspergillus oryzae TAKA protein (TAA), given in comparison with ThWA in the present invention
 maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence os that of the Asoergillus oryzae alpha amylase, sold
                                                                                                                                            ö
                                                                                                                  100.0%; Score 40; DB 4; Length 423; 100.0%; Pred. No. 17;
                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                        Methionine substitution; stability; activity; detergent;
                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                     dishwashing agents; liquifaction agents
                                                                                                                                                                                                                                                  AAR46065 standard; protein; 478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Svendsen A, Bisgard-Frantzen H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 7; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92DK-00000946.
92DK-00001503.
93DK-00000292.
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Best Local Similarity الاست
الا Conservative ، ر
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                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                               137 SSQDYFH 143
                                                                                                                                                                                                                                                                                                                                 Mutant alpha-amylase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-048855/06
                                                                                                                                                                1 SSODYFH 7
                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 478 AA;
                                                                                             Sequence 423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1992;
16-DEC-1992;
15-MAR-1993;
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                                                                                                                                                                                                                                                                                              25-MAR-2003
18-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                          03-FEB-1994
                                                                                                                                                                                                                                                                         AAR46065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                  Alpha amylase; variant; enzyme; detergent; additive; dishwashing; washing; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Bacillus derived alpha-amylase variants - having amino acid modifications to improve washing and/or dishwashing performance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Svendsen A, Thellersen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 2; Length 478; 100.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                       Aspergillus oryzae alpha amylase (mature protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 75-76; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR78270 standard; protein; 478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                           94WO-DK000370.
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                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
ses 7; Conservative
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(revised)
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                                                                                                                                                                                                                                          Aspergillus oryzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Der Zee P;
                                                                                                                                                                                                 thermostable.
                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1993;
                                                                                                                                                                                                                                                                                             WO9510603-A1
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25-MAR-2003
01-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Exervised
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Gaps

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100.0%; Score 40; DB 2; Length 478; 100.0%; Pred. No. 19; 0; Indels ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 7; Conservative

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13. 45
/label= loop 1 modification region
/label= loop 1 modification acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 7-23 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 8-18 of AAW14199 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= loop 1 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the mature form of taka-amylase from A. oryzae. This sequence was used in a method for the generation of mutant pullulanases for use in the food industry (see also AAR79026-28). The wild type pullulanase enzyme was modified by the method of the invention for enhancing the hydrophobicity of a selected site of the pullulanase. The method comprises replacement of a group in the selected site with a hydrophobic group, replacement of an amino acid with a hydrophobic amino acid, and/or insertion or deletion of a hydrophobic amino acid, and or insertion or deletion of a hydrophobic amino acid site. The method was used to produce neopullulanases Y377F, the
                                                                                                                                                                                                                                                                                       Modifying a transferase by enhancing hydrophobicity of a selected site increases transfer activity, also new mutant neo-pullulanase(\mathbf{s}).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-amylase, mature, Bacillus licheniformis, termamyl; fungamyl; Aspergillus oryzae, Bacillus amyloliquefaciens; altered property; calcium dependency; substrate binding; stability; pH optimum; thermostability; cleavage; oligosaccharide substrate; dishwashing; washing; detergent additive; fabric desizing; starch liquefaction; sweetener; ethanol production; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 478;
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/label= loop 1 modification region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB
100.0%; Pred. No. 19;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 10-11; 18pp; English
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      94JP-00288658
                                                                    93JP-00306096
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Matches 7; Conservative
                                                                                                                                (NIDE ) NEC CORP.
(EZAK ) EZAKI GLICO CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S422V and M375L
      31-OCT-1994;
                                                                    12-NOV-1993;
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         THE THEFT HE HELDER SON THE THEFT HE TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidation stable alpha amylases can be used for the simultaneous desizing and bleaching or scouring of a fabric comprising starch or starch derivatives. They exhibit a better heat stability, especially in the presence of oxidising agents. They are obtained from a parent alpha amylase by replacing one or more methionine residues with any amino acid different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or Asp. The parent alpha amylase is pref. derived from a Bacillus species, although alpha amylases of fungal origin can also be used: This sequence is the wild type (unmodified) alpha amylase of Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of an oxidation stable alpha-amylase - for simultaneous desizing and bleaching or scouring of fabrics contg. starch or starch derivs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild type; neopullulanase; B. stearothermophilus; mutant; food industry; modification; hydrophobicity; replacement insertion; deletion.
                                    fabric; starch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                       scouring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Alpna amylase; oxidation; desizing; bleaching; scouring; thermostable; methionine; Bacillus licheniformis; Bacillus amyloliquefaciens; Bacillus stearothermophilus; Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pedersen HH, Nilsson TE;
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150. .164
240. .283
439. .474
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marcher D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 SSODYFH 147
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Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                      WO9521247-A1
                                                                                                                                                                                                                                                                                                                                                                               05-OCT-1994;
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                                                                                                                                                                                                                                                                                                                    10-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toft AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR79025;
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RESULT 5

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AAR79025

Key

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Gaps

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a variant) corresponding to 325-345 of AAW14498 is deleted or replaced with a fragment corresponding to this fragment; claim 38"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the mature Aspergillus oryzae alpha-amylase (A). Variants of parent termamyl- and fungamyl-like alpha-amylases (and methods of constructing them) are claimed. Examples of variants are featured above. The variants have altered properties such as calcium dependency, substrate binding and stability. Also one or more proline or cystein residues in the variant is modified or replaced with a non-proline or non-cystein residue such as alanine. The variants can be used for (dish) washing, as detergent additives or for fabric desizing or starch liquefaction. They can also be used for the production of sweeteners and ethanol from starch. See also AAM14498-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-amylase variants and methods of production - have altered properties such as calcium dependency, substrate binding and stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alcohol; starch; dough improver; brewing; starch liquification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a fungamyl-like alpha-amylase.
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                                                                                                                                                                                                                                                                                                                                                                          Borchert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pedersen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 87-88; 171pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB84206 standard; protein; 498 AA
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                                                                                                                                                                                                                                                                                                                                                                          Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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100.0%;
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                                                                                                                                                                                                                                      95DK-00000128
                                                                                                                                                                                                                                                         95DK-00001192
95DK-00001256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-371424/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 SSODYFH 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 478 AA;
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                                                                                                                                                                                        05-FEB-1996;
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                                                                                                                                                                                                                                                         23-OCT-1995;
10-NOV-1995;
                                                                                                WO9623874-A1
                                                                                                                                                                                                                                      03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                          Svendsen A,
                                                                                                                                             08-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB84206;
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/note= "at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-206 of AAW14499; claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Increasing preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to this fragment is deleted or replaced with a fragment corresponding to 102-199 of AAW14499; claim 42"
                                                                                                                                                                                                         /label= loop 2 modification region
/label= loop 2 modification region
/note= "at least one amino acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 44-57 of AAW1449 is deleted or replaced with a
fragment corresponding to this fragment; claim 18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98. .210
/label= loop 3 modification region
/label= loop 3 modification region
/label= loop 3 modification acid residue of a parent alpha
-amylase (used as a template for a variant) corresponding
to 117-185 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label loop 3 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 121-181 of AAW14499 is
deleted or replaced with a fragment corresponding to this
                                                  32..38
/label= loop 1 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 14-15 of AAW14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                  70. 78

Jabel= loop 2 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
a variant) corresponding to 48-51 of AAW14499 is deleted
or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /notes "at least non-animo acid residue of a parent alpha -amylase (used as a template for a variant) corresponding to 195-202 of AAW14499 is deleted or replaced with a fragment corresponding to this fragment; claim 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notes "preferred region where at least one amino acid residue of a parent alpha-amylase (used as a template for a variant) corresponding to 196-198 of AAW14499 is deleted or replaced with a fragment corresponding to this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -amylase (used as a template for a variant) corresponding to 322-346 of AAW14498 is deleted or replaced with a fragment corresponding to this fragment; claim 36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= loop 8 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amylase (used as a template for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "at least one amino acid residue of a parent alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "an amino acid fragment corresponding to this region is deleted from the parent sequence of a variant
                          fragment corresponding to this fragment; claim 30"
    to 12-19 of AAW14499 is deleted or replaced with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165. .177
/label= loop 3 modification region
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|abel= loop 3 modification region
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/label= loop 8 modification region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment; claim 23"
181. .184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fungamyl; claim 43"
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                                                  Misc-difference
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Matches
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ADT89628
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                                                                                                             The present sequence represents a fungamyl-like alpha-amylase. The specification describes variants of this fungamyl-like alpha-amylase, which have an alteration in one the amino acid regions 98-110, 150-160, 160-160, 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or substitution of an amino acid or an insertion of an amino acid downstream of a particular position. The variants retain alpha-amylase activity, and have better heat stability and/or stability at acidic ph, relative to wild-type enzyme. The variants can therefore be used at higher comperatures (more efficient conversion or faster reaction, and have reduced need for cooling and reduced risk of contamination). The variants may also be used in conjunction with other enzymes, particularly of high maltose content, or alcohol, from starch; as dough improver for baked goods; in brewing, to increase fermentability of the wort; and for liquefaction of starch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing heterologous biological substance comprises culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance and recovering heterologous biological
                                             New variant of Fungamyl-like alpha-amylase, useful for production of maltose syrups, includes mutations that improve stability against heat
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                      Score 40; DB 4; Length 498;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus niger neutral alpha-amylase A (amyA) protein.
                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glucoamylase; glaA; amyA; alpha-amylase A; enzyme.
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                             Claim 1; Page 42-45; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADT89632 standard; protein; 498 AA.
                                                                                                                                                                                                                                                                                                                                    h 100.0%;
Similarity 100.0%;
7; Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                            161 SSQDYFH 167
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            WPI; 2001-367478/38
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   1 SSQDYFH 7
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                       N-PSDB; AAF90208
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                                                                                                                                                                                                                                                                                                                Sequence 498 AA;
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The present invention relates to a method of producing heterologous hological substance. The method involves culturing mutant of wild-type haspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide heterologous biological substance and second nucleotide heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase A (amyA) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method of producing heterologous biological substance. The method involves culturing mutant of wild-type Aspergillus niger strain in medium suitable for producing heterologous biological substance, where mutant strain comprises first nucleotide sequence encoding heterologous biological substance and second nucleotide sequence comparising medification of glucosmylase (glash) and recovering heterologous biological substance. The present sequence is the Aspergillus niger neutral alpha-amylase B (amyB) protein.
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                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 8; Length 498; 100.0%; Pred. No. 20; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus niger neutral alpha-amylase B (amyB) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
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100.0%; Pred. No. 20;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADT89628 standard; protein; 499 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2003; 2003US-0459902P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 SSQDYFH 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-708545/69.
N-PSDB; ADT89627.
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Connelly M, Brody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SSODYFH
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                                                                                                                                                                                                                                                                                                       Sequence 498 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADT89628;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562) isolated from a T. lanuginosus gene library. The recombinant enzyme (54-60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7 and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermophilic alpha-amylase with activity range of 60-80 degrees C -derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs and bakery prods. esp. bread.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, cytokine; cell proliferation; cell differentiation; gene therapy, vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS
                                                                                                                                                                                                       Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37;
Pred. No. 7
                                                                                                                                                                                                                                                                                                             1. .18
/label= Sig_peptide
                                                                                                                                                                                                                                               Thermomyces lanuginosus; CBS 224.63
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                   AAR88212 standard; protein; 493 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 36-38; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 22339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA008447 standard; protein; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-EP002607.
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                                                                                                   (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 NSQDYFH 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-087673/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DANI-) DANISCO AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SSQDYFH 7
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                                                                                                                                                                 Alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Michelsen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                      WO9601323-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                   16-OCT-2003
03-APR-1996
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                                                             AAR88212;
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                                                                                                                                                                                                                                                                                                           Peptide
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  AAR88212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA008447
                         %XGCCCCCCCX8X4444X64X1X4X4X4X4X44444X8X8X6CCCCCCCCCCCCCCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes polynucleotides which encode processing enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose carginesase, or glucoamylase) that are optimised for expression in plants. Compose the polynucleotides encode mesophilic, thermophilic or hyperthermophilic. The polynucleotides encode mesophilic, thermophilic or hyperthermophilic or processing enzymes, which are activated under suitable conditions to act upon the desired substrate. Also described are self-processing transgenic composition that facilitates plant and grain comparing. Also described is a method (M) for converting starch to starch-derived products in a transformed plant part (TPP), by activating the starch-derived products of a transformed plant (TP) can be used to composite maltodextrin. A transformed plant (TPP) can be used to produce for ethanol and fermented beverages. (M) eliminates the need to recovery of starch-derived products. The present sequence represents alpha-amylase/glucoamylase fusion process. The present sequence represents calpha-amylase/glucoamylase fusion procein, which is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotide encoding hyperthermophilic processing enzymes e.g. alpha-amylase, useful for producing plant to produce food products having improved taste or fermentable substrates for ethanol.
                                                                                                                                                                                                                                                                Self-processing plant; plant; processing enzyme; alpha-amylase; grain; pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase; mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch; maltodextrin; ethanol; fermentation; beverage; enzyme.
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                                                                                                                                                                                                                          Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Batie CJ, Chen W,
                                                                                                 ABP96630 standard; protein; 1095 AA.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Aspergillus shirousami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Basu SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 SSQDYFH 147
162 SSQDYFH 168
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Synthetic.

ABP96630;

RESULT 10

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RESULT 11

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99US-0127462P.
99US-0128234P.
99US-0128714P.
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990S-0132048P.
990S-0132407P.
990S-0132484P.
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99US-0132863P.
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99US-0139763P.
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99US-0134941P.
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99US-0141287P
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21-APR-1999

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28-APR-1999

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10-APR-1999

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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
20-MAY-1999;
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07-MAY-1999;
11-MAY-1999;
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08-JUN-1999;
10-JUN-1999;
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11-JUN-1999
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24-MAY-1999
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27-MAY-1999
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                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, laukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification, signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                  Claim 20; SEQ ID NO 22339; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                85.0%; Score 34; DB 4; Length 52;
85.7%; Pred. No. 28;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 44675.
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99US-0123180P.
99US-0123548P.
99US-0125788P.
                                                 26-FEB-2001; 2001WO-US004927.
                                                                        28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409
                                                                                                                              Tang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                   WPI; 2001-514838/56.
N-PSDB; AAI88378.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                         (HYSE-) HYSEQ INC.
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          WO200164835-A2
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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                               07-SEP-2001
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        99US-0144331 P

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        19-JUL-1999 j
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        99US-0144332 P

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        19-JUL-1999 j
        99US-0144332 P

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        20-JUL-1999 j
        99US-01451484 P

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        20-JUL-1999 j
        99US-0145184 P

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        20-JUL-1999 j
        99US-0145318 P

        PR
        20-JUL-1999 j
        99US-0145318 P
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 7.5e+02;
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Pred. No. 7.8e+02;
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